

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:56:54 ; Search time 3238.46 Seconds
(without alignments)
4666.271 Million cell updates/sec

Title: US-10-081-969-93
Perfect score: 397
Sequence: 1 cccctgtggtccctgca.....tggccccggccacccccgcg 397

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	95.4	24.0	1675	9	AG360980	Mus muscu
C 2	90.8	22.9	935	9	CNS006XK	AL066051 Drosophil
C 3	90.8	22.9	1146	5	BU955946	AGENCOURT
C 4	90.4	22.8	1020	6	CA792179	AGENCOURT
C 5	87.6	22.1	967	5	BQ678596	AGENCOURT
C 6	87.6	22.0	995	5	BQ939901	AGENCOURT
C 7	87.2	22.0	944	5	BU516035	AGENCOURT
C 8	87	21.9	807	7	CF149720	AGENCOURT
C 9	87	21.9	963	5	BU503665	AGENCOURT
C 10	87	21.9	972	5	BO900341	AGENCOURT
C 11	86.4	21.8	925	9	CNS0081P	AL053013 Drosophil
C 12	86.2	21.7	982	9	CL473807	AL066051 Drosophil
C 13	86.2	21.7	1203	9	CNS015Y4	AL066051 Drosophil
C 14	85.8	21.6	1162	5	BQ051092	AGENCOURT
C 15	85.6	21.6	1088	5	BU505362	AGENCOURT
C 16	85.4	21.5	1048	5	BU529717	AGENCOURT
C 17	85.2	21.5	671	8	BH997981	BU955946
C 18	84.8	21.4	1136	5	BQ943816	AGENCOURT
C 19	84.6	21.3	943	4	BM415351	OP20425 M
C 20	84.4	21.3	1135	9	AG383043	Mus muscu
C 21	84.2	21.2	776	9	CNS010Y3	AL099352 Drosophil
C 22	84.2	21.2	926	9	CL497807	SAIL 547
C 23	84.2	21.2	1021	5	BQ434910	AGENCOURT
C 24	84.2	21.2	1057	5	BU526464	AGENCOURT

C 25	83.8	21.1	932	9	CNS0072Q	AL066742 Drosophil
C 26	83.6	21.1	986	9	CL473390	SAIL 199
C 27	83.6	21.1	1080	8	AQ893056	HS 4832 A
C 28	83.6	21.1	1462	9	AG411877	Mus muscu
C 29	83.4	21.0	918	4	BG809598	mgc001xb
C 30	83.4	21.0	1141	9	CL082639	CH216-168
C 31	83.4	21.0	1273	4	BM562099	AGENCOURT
C 32	83.4	21.0	1474	8	BZ569821	msb2_1034
C 33	83.2	21.0	825	9	AG081347	Pan trogl
C 34	83.2	21.0	1169	4	BM549879	AGENCOURT
C 35	82.8	20.9	1190	5	BO673485	AGENCOURT
C 36	82.8	20.9	1692	9	AG396765	Mus muscu
C 37	82.6	20.8	942	5	BQ681469	AGENCOURT
C 38	82.6	20.8	974	9	AG071677	Pan trogl
C 39	82.6	20.8	985	5	BQ672571	AGENCOURT
C 40	82.6	20.8	1048	5	BUI46089	AGENCOURT
C 41	82.4	20.8	1523	9	AG448267	Mus muscu
C 42	82.4	20.8	1619	9	AG435648	Mus muscu
C 43	82.4	20.8	1822	9	AG435170	Mus muscu
C 44	82.2	20.7	966	9	CL462945	SAIL 1173
C 45	82.2	20.7	1830	9	CL078620	CH216-151

ALIGNMENTS

RESULT 1
AG360980/c
LOCUS AG360980 1675 bp DNA linear GSS 03-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMG01-161J23.T7, genomic survey sequence.
ACCESSION AG360980
VERSION AG360980.1 GI:47972185
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
REFERENCE 2 (bases 1 to 1675)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Sushiro-cho,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Taikuba Institute, Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY : pBACe3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
FEATURES
source
1..1675
Location/Qualifiers
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMG01-161J23.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMG01 Mouse Male BAC Library"

ORIGIN		/mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR14N09" /clone_lib="RPC1-98" /note="end : T7"	
Query Match		22.9%;	Score 90.8; DB 9; Length 935;
Best Local Similarity		35.6%;	Pred. No. 5.4e-07;
Matches 116;		Conservative 84;	Mismatches 126; Indels 0; Gaps 0;
QY	37	GGCGCGGGGGGAAAGCGCGCCAGACCCCGGGTTCGGCGGAGCGAGCTCGGCTGT 96	
DB	934	GSCGGGGSGSSGSGCGGCGGSGGSCCGCGCCGCGCGCGCGCGCGCGCGCGCG 875	
QY	97	CGGGGCGAGCGGGCTCCAGTTCGCGGCGACAGCGCCAGAGCGCGCTTCCC 156	
DB	874	SCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 815	
QY	157	ACGTGGCGGAGGACATGGGGACCCGGGACCCCGTCTGCGCCCTTACCTTCCAGCTCGC 216	
DB	814	CGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 755	
QY	217	CTCTCGCGCGAGACCCCGCGCGCTCCGACACCCCTCCCGGTCGCCGCGCGCCCTC 276	
DB	754	GSCSSSGSGSGCGSGGSGGSGCGSGCGCGCGSGGSGGCGCGCGCGCGCGCGCGSG 695	
QY	277	CGGGCGCTCCAGCCCTCCCTTCTTCCTTCGCGGCGCCCGCGCTCTCTCTCGGCGCGGAG 336	
DB	694	CGCGGSGSGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 635	
QY	337	TTTCAGGCGAGCGTGTGCTCTGCTGC 362	
DB	634	CCSCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 609	
RESULT 3		BU955946/c 1146 bp mRNA linear EST 21-OCT-2002	
LOCUS		AGENCOURT 10621110 NIH MGC 107 Homo sapiens cDNA clone	
DEFINITION		IMAGE:6729411 5', mRNA sequence.	
ACCESSION		BU955946	
VERSION		BU955946.1 GI:24185518	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 1146)	
TITLE		NIH-MGC http://mgs.nci.nih.gov/.	
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT		Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM3052 row: j column: 02 High quality sequence stop: 163. Location/Qualifiers 1..1146 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6729411" /tissue_type="adenocarcinoma, cell line" /lab_hosts="DH10B (phage-resistant)" /clone_lib="NIH_MGC_107" /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;	
FEATURES		source	

ORIGIN		Query Match		24.0%;	Score 95.4; DB 9; Length 1675;
Best Local Similarity		51.9%;	Pred. No. 7.3e-08;		
Matches 204;		Conservative 0;	Mismatches 189; Indels 0; Gaps 0;		
QY	2	CCTCGTGGGTCTCCGACCTGGAGCGCGGCGCGGCGGGAAGCGCGGCC 61			
DB	1670	CCCCCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1611			
QY	62	CAGACCCCGGGTTCGCGCGGAGCAGCTGCGCTGTCGGGGCCAGGCGCGGGTTCACAGTGG 121			
DB	1610	GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1551			
QY	122	ATTTCGCGGCGCAGACCGCCAGGACGCGCTTCCACAGTGGCGGAGGACTGGGACCGG 181			
DB	1550	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1491			
QY	182	GGCACCGCTCTGCGCGCTTCACTTCCAGTCCGCTCTCTCGCGGAGCGCGCGCGCGCT 241			
DB	1490	CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1431			
QY	242	CCCGACCTCTCCGGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 301			
DB	1430	CCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1371			
QY	302	CTTTCGCGGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGAGCGCTGCTCTGCTG 361			
DB	1370	GC CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1311			
QY	362	CGCACGTGGGAGCCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394			
DB	1310	GC CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1278			
RESULT 2		CNS006XK/c 935 bp DNA linear GSS 03-JUN-1999			
LOCUS		Drosophila melanogaster genome survey sequence T7 end of BAC #			
DEFINITION		BACR14N09 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION		AL066051			
VERSION		AL066051.1 GI:4945019			
KEYWORDS		GSS.			
SOURCE		Drosophila melanogaster (fruit fly)			
ORGANISM		Drosophila melanogaster			
REFERENCE		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
AUTHORS		1 (bases 1 to 935)			
TITLE		Genoscope.			
JOURNAL		Direct Submission			
COMMENT		Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm . Location/Qualifiers 1..935 /organism="Drosophila melanogaster"			
FEATURES		source			

Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 22.9%; Score 90.8; DB 5; Length 1146;
Best Local Similarity 49.9%; Pred. No. 5.3e-07;
Matches 179; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

QY 38 GCGCGCGGCGGGAAGCGCGGCCAGACCCCGGGTTCGCGCGAGCAGTGGCTTTC 97
DB 945 GCGCGCGGCGGCGGTCGCGCGCGCGGCGGCGCGCGCGCGCGCGCGCGCGCG 886

QY 98 GGGGCGAGCGCGGCTCCAGTGGATTTCGCGGCGACAGCGCCAGGACCGGCTTCCCA 157
DB 895 GCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 826

QY 158 CGTGGCGGAGGACTGGGGACCGCGGCGACCGGCTTTCAGCTTCCAGCTTCCGCG 217
DB 825 GCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 766

QY 218 TCCTCCCGCGGACCGCGCGCGCGTCCGACCGCTCCCGGGTCCCGCGCGCGCGCGTCC 277
DB 765 CCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 706

QY 278 GGGGCGTCCGAGCGCGCGCGCGTCCGACCGCTCCCGGGTCCCGCGCGCGCGCGTCC 337
DB 705 NNCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 646

QY 338 TTCAGGCGCGCGTGGTCTGTGGCGACGTTGGGAAGCGCGCGCGCGCGCGCGCGCG 396
DB 645 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 587

RESULT 4

CA792179/c
LOCUS CA792179
DEFINITION AGENCOURT_10316321 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
IMAGE:5155002 5', mRNA sequence.

CA792179.1 GI:26039911
EST.
Xenopus laevis (African clawed frog)

ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE
1 (bases 1 to 1020)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

UNPUBLISHED (1997)
CONTACT: Robert Strausberg, Ph.D.
EMAIL: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLNL1383 row: m column: 19
High quality sequence stop: 263.
Location/Qualifiers

FEATURES

source
1..1020
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="caxon:8355"
/clone="IMAGE:5155002"

/tissue_type="embryo (stage 10)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Emb1"
/note=Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."

ORIGIN

Query Match 22.8%; Score 90.4; DB 6; Length 1020;
Best Local Similarity 50.0%; Pred. No. 6.3e-07;
Matches 196; Conservative 0; Mismatches 196; Indels 0; Gaps 0;

QY 5 CGCTGGGCTCCCTGCACCTTGGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 64
DB 823 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 764

QY 65 ACCCGCGGTCGCGCGCGGAGCAGCTGGCTGTTCGGGGCCAGCGCGGCTCCAGTGGATT 124
DB 763 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 704

QY 125 CGCGGCGACAGACCGCGCGCGCGCGCTTCCACGTGGCGGAGGAGCTGGGGACCGCGCG 184
DB 703 GGCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 644

QY 185 ACCCGTCTTGCCTTTCACCTTCCAGTTCGCGCTTCTCCGCGCGCGCGCGCGCGTCC 244
DB 643 CCCCNCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 584

QY 245 GACCGCTCCCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTCTCT 304
DB 583 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 524

QY 305 TCCCGCGCGCGCGCGCTCTCTCTCGCGCGCGCGGAGTTTCAGGCGAGCGTGTCTGTCTG 364
DB 523 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 464

QY 365 ACCTGGGAAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
DB 463 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 432

RESULT 5

BQ678596/c
LOCUS BQ678596
DEFINITION AGENCOURT_8196706 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6263404
5', mRNA sequence.

ACCESSION
BQ678596
VERSION BQ678596.1 GI:21791275
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 967)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
UNPUBLISHED (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNM2427 row: e column: 05
High quality sequence stop: 399.
Location/Qualifiers

FEATURES

source
1..967
/organism="Homo sapiens"
/mol_type="mRNA"

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14042 row: j column: 07
High quality sequence stop: 430.
Location/Qualifiers
1. .563
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6491334"
/tissue_type="retina"
/lab_host="NIH MGC 94"
/clone_lib="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES
source
1. .963
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6331356"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 130"
/note="Organ: oocyte; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 87; DB 5; Length 963;
Best Local Similarity 47.7%; Pred. No. 2.6e-06;
Matches 189; Conservative 0; Mismatches 207; Indels 0; Gaps 0;
QY 1 CCTCTGCTGGTCTGTGACCTGGAGCGGAGCGGCGGGGGAGCGCGGC 60
DB 908 CCGCGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 849
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGTGCCTGTCGGGGCAGCGCGGCTCC 120
DB 848 GCNCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 789
QY 121 GATTTCGGGGCACAGACGCCCGCGCGCTTCCACAGTGGCGAGGACCTGG 180
DB 788 GGGCGCGNGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 729
QY 181 GGGCAGCCCTCTGCGCCCTTACCTTCAGCTCGGCTCTCTCGGCGGACCC 240
DB 728 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 669
QY 241 TCCGACCCCTCCCGGGTCCCGGGCCAGCCCTTCCCGGGCTCCCGCCCTT 300
DB 668 NNCGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 609
QY 301 CTTTTCGGCGCGCGCGCGCGCTCTCTCTCGCGCGCGAGTTTCAGGCAGCG 360
DB 608 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 549
QY 361 GGCAGCTGGAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
DB 548 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 513

RESULT 10
BQ900341/c
LOCUS
DEFINITION
AGENCY: 8750450 NIH_MGC_130 Mus musculus cDNA clone IMAGE:633156
5', mRNA sequence.
ACCESSION
BQ900341
VERSION
BQ900341.1 GI:2292355
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 972)
REFERENCE
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13791 row: o column: 13
High quality sequence stop: 413.
Location/Qualifiers
1. .972
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6331356"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 130"
/note="Organ: oocyte; Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.9%; Score 87; DB 5; Length 972;
Best Local Similarity 47.3%; Pred. No. 2.6e-06;
Matches 183; Conservative 0; Mismatches 204; Indels 0; Gaps 0;
QY 10 GCGTCCCTGCACCTTGGGAGCGCGAGCGCGCGGGGAGCGCGGCGCGACCC 69
DB 769 GCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 710
QY 70 CGGGTCCCGCGGAGCAGCTGGCTGTGCGGGGCGAGCGCGGGCTCCAGTTCGG 129
DB 709 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 650
QY 130 GCACAGAGCGCGAGACCGCGCTTCCAGTGGCGGAGCTGGGAGCGCGGAC 189
DB 649 GCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 590
QY 130 TCTTCCCTTTCACCTTCCAGTTCGCTCTCTCGCGGAGACCGCGCGCGCG 249
DB 589 CCGNNCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 530
QY 250 CTCGGGGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 309
DB 529 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
QY 310 GCGCGCGCGCTCTCTCTCGCGGCGAGTTTCAGGCAGCGCTGCGTCTGCG 369
DB 469 CCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 410
QY 370 GGAAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 396
DB 409 NNGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 383

RESULT 11
CNS0091P
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL053013
VERSION
AL053013.1 GI:4934461
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 06:08:24 ; Search time 507.69 Seconds
(without alignments)
4738.760 Million cell updates/sec

Title: US-10-081-969-93

Perfect score: 397

Sequence: 1 cccctgtggcgtccctgca.....tggcccccggcaccaccccgcg 397

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	397	100.0	397	15	US-10-081-969-93
2	397	100.0	4293	18	US-10-456-830-1
3	397	100.0	4321	17	US-10-325-810-6
4	397	100.0	15418	9	US-09-783-203-1
5	397	100.0	15418	9	US-09-994-427A-1
6	397	100.0	15418	10	US-09-995-419A-1
7	397	100.0	15418	14	US-10-141-220-1
8	397	100.0	15418	14	US-10-023-969-1
9	397	100.0	15418	14	US-10-206-447-1
10	397	100.0	15418	17	US-10-674-836-1
11	397	100.0	15418	18	US-10-811-012-1
12	397	100.0	15418	18	US-10-811-012-1
13	397	100.0	15418	18	US-10-811-012-1
14	397	100.0	15418	18	US-10-811-012-1
15	397	100.0	15418	18	US-10-811-012-1
16	397	100.0	15418	18	US-10-811-012-1
17	397	100.0	15418	18	US-10-811-012-1
18	397	100.0	15418	18	US-10-811-012-1
19	397	100.0	15418	18	US-10-811-012-1
20	397	100.0	15418	18	US-10-811-012-1
21	397	100.0	15418	18	US-10-811-012-1
22	397	100.0	15418	18	US-10-811-012-1
23	397	100.0	15418	18	US-10-811-012-1
24	397	100.0	15418	18	US-10-811-012-1
25	397	100.0	15418	18	US-10-811-012-1
26	397	100.0	15418	18	US-10-811-012-1
27	397	100.0	15418	18	US-10-811-012-1
28	397	100.0	15418	18	US-10-811-012-1
29	397	100.0	15418	18	US-10-811-012-1
30	397	100.0	15418	18	US-10-811-012-1
31	397	100.0	15418	18	US-10-811-012-1
32	397	100.0	15418	18	US-10-811-012-1
33	397	100.0	15418	18	US-10-811-012-1
34	397	100.0	15418	18	US-10-811-012-1
35	397	100.0	15418	18	US-10-811-012-1
36	397	100.0	15418	18	US-10-811-012-1
37	397	100.0	15418	18	US-10-811-012-1
38	397	100.0	15418	18	US-10-811-012-1
39	397	100.0	15418	18	US-10-811-012-1
40	397	100.0	15418	18	US-10-811-012-1
41	397	100.0	15418	18	US-10-811-012-1
42	397	100.0	15418	18	US-10-811-012-1
43	397	100.0	15418	18	US-10-811-012-1
44	397	100.0	15418	18	US-10-811-012-1
45	397	100.0	15418	18	US-10-811-012-1

12	395.4	99.6	5126	19	US-10-840-455-1	Sequence 1, Appli
13	395.4	99.6	11276	19	US-10-840-455-3	Sequence 3, Appli
14	395.4	99.6	26414	19	US-10-840-455-43	Sequence 43, Appli
15	395.4	99.6	51552	9	US-09-733-294A-30	Sequence 30, Appli
16	376.4	94.8	378	14	US-10-212-667-1	Sequence 1, Appli
17	354.2	89.2	35871	9	US-09-956-335-2	Sequence 2, Appli
18	354.2	89.2	35978	9	US-09-956-335-1	Sequence 1, Appli
19	351	88.4	1677	9	US-09-956-335-3	Sequence 3, Appli
20	341.8	86.1	4335	18	US-10-877-124-6	Sequence 6, Appli
21	341.8	86.1	4335	18	US-10-877-124-6	Sequence 6, Appli
22	341.8	86.1	4335	19	US-10-877-146-6	Sequence 6, Appli
23	338.8	85.3	4200	14	US-10-044-692-6	Sequence 6, Appli
24	338.8	85.3	4200	15	US-10-044-539-6	Sequence 6, Appli
25	310	78.1	460	18	US-10-456-830-6	Sequence 8, Appli
26	298.2	75.1	314	9	US-09-916-510A-8	Sequence 8, Appli
27	298.2	75.1	314	17	US-10-376-630-8	Sequence 8, Appli
28	297.2	74.9	361	18	US-10-456-830-8	Sequence 8, Appli
29	297.2	74.9	381	18	US-10-456-830-9	Sequence 9, Appli
30	295	74.3	298	17	US-10-674-836-17	Sequence 17, Appli
31	273.8	69.0	4356	17	US-10-240-589C-144	Sequence 144, App
32	260.4	65.6	327	19	US-10-483-289A-8	Sequence 8, Appli
33	259	65.2	293	19	US-10-483-289A-5	Sequence 5, Appli
34	256.4	64.6	261	10	US-09-932-581-24	Sequence 24, Appli
35	256.4	64.6	261	16	US-10-338-294-24	Sequence 24, Appli
36	256.4	64.6	261	19	US-10-863-075-24	Sequence 24, Appli
37	256.4	64.6	295	15	US-10-140-763A-12	Sequence 12, Appli
38	256.4	64.6	5928	10	US-09-932-581-25	Sequence 25, Appli
39	256.4	64.6	5928	16	US-10-338-294-25	Sequence 25, Appli
40	256.4	64.6	5928	19	US-10-863-075-25	Sequence 25, Appli
41	244	61.5	245	15	US-10-081-969-94	Sequence 94, Appli
42	244	61.5	955	15	US-10-081-969-17	Sequence 17, Appli
43	216.4	54.5	240	15	US-10-140-763A-13	Sequence 13, Appli
44	199.8	50.3	403	15	US-10-081-969-21	Sequence 21, Appli
45	181.2	45.6	4356	17	US-10-240-589C-143	Sequence 143, App

ALIGNMENTS

RESULT 1

US-10-081-969-93

; Sequence 93, Application US/10081969

; Publication No. US20030104625A1

; GENERAL INFORMATION:

; APPLICANT: Cheng, Cheng

; APPLICANT: Clarke, Lori

; APPLICANT: Connelly, Sheila

; APPLICANT: Ennist, David

; APPLICANT: Forry-Schaudies, Suzanne

; APPLICANT: Gorziglia, Mario

; APPLICANT: Hallenbeck, Paul

; APPLICANT: Hay, Carl

; APPLICANT: Jakubczak, John

; APPLICANT: Kaleko, Michael

; APPLICANT: Phipps, Sandrina

; APPLICANT: Police, Seshidhar

; APPLICANT: Ryan, Patricia

; APPLICANT: Steward, David

; APPLICANT: Xie, Yufeng

; TITLE OF INVENTION: No. US20030104625A1el Oncolytic Adenoviral Vectors

; FILE REFERENCE: 4-31704A/GTI

; CURRENT APPLICATION NUMBER: US/10/081.969

; PRIOR FILING DATE: 2002-02-22

; PRIOR APPLICATION NUMBER: US 60/270,922

; PRIOR FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: US 60/295,037

; PRIOR FILING DATE: 2001-06-01

; PRIOR APPLICATION NUMBER: US 60/348,670

; PRIOR FILING DATE: 2000-01-14

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 93

; LENGTH: 397


```

; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(397)
; OTHER INFORMATION: A 397 bp fragment of the hTERT promoter
US-10-081-969-93

Query Match      100.0%; Score 397; DB 15; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGCTGGCTCCCTGACACCTTGGAGCGGAGCGCGCGCGGGAAGCGCGGC 60
DB 1 CCTCTGCTGGCTCCCTGACACCTTGGAGCGGAGCGCGCGCGGGAAGCGCGGC 60
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGCGGCTCCAGTG 120
DB 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGCGGCTCCAGTG 120
QY 121 GATTCCGGGGCACAGACGCCAGGACCGCGCTTCCACGCTGGCGGAGGACTGGGGACCC 180
DB 121 GATTCCGGGGCACAGACGCCAGGACCGCGCTTCCACGCTGGCGGAGGACTGGGGACCC 180
QY 181 GGSCACCCGCTCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCCG 240
DB 181 GGSCACCCGCTCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCCG 240
QY 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCTCCCGCTTCCCGCTT 300
DB 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCTCCCGCTTCCCGCTT 300
QY 301 CCTTTCCGGGGCCCGCCCTCTCTCTCGCGCGGCGAGTTTCAGGACGCTGGTCTCTGCT 360
DB 301 CCTTTCCGGGGCCCGCCCTCTCTCTCGCGCGGCGAGTTTCAGGACGCTGGTCTCTGCT 360
QY 361 GCGCAGCTGGGAAGCCCTGCGCCCGCGCACCCCGCGG 397
DB 361 GCGCAGCTGGGAAGCCCTGCGCCCGCGCACCCCGCGG 397

RESULT 2
US-10-456-830-1
; Sequence 1, Application US/10456830
; Publication No. US20040248246A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as
; represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Horikawa, Izumi
; APPLICANT: Barrett, J. Carl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING DIFFERENTIAL EXPRESSION
; FILE REFERENCE: 4239-63008
; CURRENT APPLICATION NUMBER: US/10/456,830
; CURRENT FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3545)..(3609)
; OTHER INFORMATION: Region identical to HBV integration site in huH-4 cell line
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3729)..(3734)
; OTHER INFORMATION: Upstream E-box
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3915)..(3916)
; OTHER INFORMATION: Major transcription initiation site

```

```

; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (3916)..(3970)
; OTHER INFORMATION: 5' untranslated region of mRNA
; FEATURE:
; NAME/KEY: protein bind
; LOCATION: (3937)..(3942)
; OTHER INFORMATION: Downstream E-box
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3971)..(4189)
; OTHER INFORMATION: Exon 1
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: (4029)..(4050)
; OTHER INFORMATION: GW2 primer binding site
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (4190)..(4293)
; OTHER INFORMATION: Intron 1
US-10-456-830-1

Query Match      100.0%; Score 397; DB 18; Length 4293;
Best Local Similarity 100.0%; Pred. No. 8.5e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGCTGGCTCCCTGACACCTTGGAGCGGAGCGCGCGGGAAGCGCGGC 60
DB 3574 CCTCTGCTGGCTCCCTGACACCTTGGAGCGGAGCGCGCGGGAAGCGCGGC 3633
QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGCGGCTCCAGTG 120
DB 3634 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGGGGGCGAGCGCGGCTCCAGTG 3693
QY 121 GATTCCGGGGCACAGACGCCAGGACCGCGCTTCCACGCTGGCGGAGGACTGGGGACCC 180
DB 3694 GATTCCGGGGCACAGACGCCAGGACCGCGCTTCCACGCTGGCGGAGGACTGGGGACCC 3753
QY 181 GGGCACCCGCTCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCCG 240
DB 3754 GGGCACCCGCTCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCCG 3813
QY 241 TCCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCTCCCGGCGCTCCCGCTT 300
DB 3814 TCCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCTCCCGGCGCTCCCGCTT 3873
QY 301 CCTTTCCGGGGCCCGCCCTCTCTCTCGCGGCGGAGTTTCAGGACGCTGGTCTCTGCT 360
DB 3874 CCTTTCCGGGGCCCGCCCTCTCTCTCGCGGCGGAGTTTCAGGACGCTGGTCTCTGCT 3933
QY 361 GCGCAGCTGGGAAGCCCTGCGCCCGCGCACCCCGCGG 397
DB 3934 GCGCAGCTGGGAAGCCCTGCGCCCGCGCACCCCGCGG 3970

RESULT 3
US-10-325-810-6
; Sequence 6, Application US/10325810
; Publication No. US20030204069A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

```

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: -
LOCATION: 1..4321
OTHER INFORMATION: /note= "genomic DNA insert of pGRN14"

FEATURE:

NAME/KEY: intron
LOCATION: 2702..2804
OTHER INFORMATION: /note= "intron 1"

FEATURE:

NAME/KEY: intron
LOCATION: 4160..4313
OTHER INFORMATION: /note= "intron 2"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-325-810-6

Query Match 100.0%; Score 397; DB 17; Length 4321;
Best Local Similarity 100.0%; Pred. No. 8.5e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCGCTGGGCTCCCTGCACCTCGGAGCGGAGCGCGCGCGGCGGGAAGCGCGGC 60
Db 2086 CCCTCGCTGGGCTCCCTGCACCTCGGAGCGGAGCGCGCGCGGCGGGAAGCGCGGC 2145

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTCGGGGCGAGCCCGGGGCTCCCAATG 120
Db 2146 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTCGGGGCGAGCCCGGGGCTCCCAATG 2205

Qy 121 GATTGGGGGCACAGACGCCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 2206 GATTGGGGGCACAGACGCCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 2265
Qy 181 GGGCACCGCTCTCGCCCTTCCACTTCCAGTCCGCTCCCTCCGCGGAGCCCGCGCGG 240
Db 2266 GGGCACCGCTCTCGCCCTTCCACTTCCAGTCCGCTCCCTCCGCGGAGCCCGCGCGG 2325
Qy 241 TCCGACCCCTCCCGGGTCCCGGCCAGACCCCTCCGCGGCTCCACAGCCCTCCCTTT 300
Db 2326 TCCGACCCCTCCCGGGTCCCGGCCAGACCCCTCCGCGGCTCCACAGCCCTCCCTTT 2385
Qy 301 CTTTTCGCGCGCCCGCCCTCTCTCGCGGCGAGTTTTCAGGAGCGCTGCGTCTGCT 360
Db 2386 CTTTTCGCGCGCCCGCCCTCTCTCGCGGCGAGTTTTCAGGAGCGCTGCGTCTGCT 2445
Qy 361 GCGACAGTGGGAAGCCCTGGGCCCGGCCACCCCGCGG 397
Db 2446 GCGACAGTGGGAAGCCCTGGGCCCGGCCACCCCGCGG 2482

RESULT 4

US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. US20020098582A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match 100.0%; Score 397; DB 9; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCGCTGGGCTCCCTGCACCTTGGGAGCGGAGCGCGCGGCGGGAAGCGCGGC 60
Db 13148 CCCTCGCTGGGCTCCCTGCACCTTGGGAGCGGAGCGGCGCGGCGGGAAGCGCGGC 13207

Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGGCGCTGTGCGGGGCGAGCGCGGGTCCCAATG 120
Db 13208 CCAGACCCCGGGTCCCGCGGAGCAGCTGGCGCTGTGCGGGGCGAGCGCGGGTCCCAATG 13267

Qy 121 GATTGGGGGCACAGACGCCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGGGGGCACAGACGCCAGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327

Qy 181 GGGCACCGCTCTCGCCCTTCCACTTCCAGTCCGCTCCCTCCGCGGAGCCCGCGCGG 240
Db 13328 GGGCACCGCTCTCGCCCTTCCACTTCCAGTCCGCTCCCTCCGCGGAGCCCGCGCGG 13387

Qy 241 TCCGACCCCTCCCGGGTCCCGGCCAGACCCCTCCGCGGCTCCACAGCCCTCCCTTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCCAGACCCCTCCGCGGCTCCACAGCCCTCCCTTT 13447

Qy 301 CTTTTCGCGCGCCCGCCCTCTCTCGCGGCGAGTTTTCAGGAGCGCTGCGTCTGCT 360
Db 13448 CTTTTCGCGCGCCCGCCCTCTCTCGCGGCGAGTTTTCAGGAGCGCTGCGTCTGCT 13507

QY 1 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 13207
QY 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 13267
QY 121 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 180
Db 13268 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 13327
QY 181 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 240
Db 13328 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 13387
QY 241 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTCCGCGGCGTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTCCGCGGCGTCCAGCCCTCCCTT 13447
QY 301 CCTTTCGCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 360
Db 13448 CCTTTCGCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 13507
QY 361 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 397
Db 13508 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 13544

RESULT 8

US-10-023-969-1
; Sequence 1, Application US/10023969
; Publication No. US20030095989A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Lebowksi, Jane
; TITLE OF INVENTION: Chimeric Cytolytic Viruses for Cancer Treatment
; FILE OF INVENTION: 084,002
; CURRENT APPLICATION NUMBER: US/10/023,969
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/256,418
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-969-1

Query Match 100.0%; Score 397; DB 14; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 13207
QY 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 13267
QY 121 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 180
Db 13268 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 13327
QY 181 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 240
Db 13328 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 13387
QY 241 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTCCGCGGCGTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTCCGCGGCGTCCAGCCCTCCCTT 13447

Db 13388 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTCCGCGGCGTCCAGAGCCCTCCCTT 13447
QY 301 CCTTTCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 360
Db 13448 CCTTTCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 13507
QY 361 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 397
Db 13508 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 13544

RESULT 9

US-10-206-447-1
; Sequence 1, Application US/10206447
; Publication No. US20030099616A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Irving, John
; APPLICANT: Karpf, David
; APPLICANT: Schiff, Michael
; TITLE OF INVENTION: DUAL SPECIFICITY TUMOR KILLING VECTORS DRIVEN BY THE TELOMERASE P
; FILE OF INVENTION: 085/002
; CURRENT APPLICATION NUMBER: US/10/206,447
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/308,029
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-206-447-1

Query Match 100.0%; Score 397; DB 14; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 60
Db 13148 CCCTCGCTGGCGTCCCTGCAACCTGGAGCGGAGCGGCGCGGGCGGGGAGCGCGGC 13207
QY 61 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 120
Db 13208 CCAGACCCCGGGTCCGCGCCCGAGCAGCTGCGTGTGCGGGCCAGGCGGCGTCCCACTG 13267
QY 121 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 180
Db 13268 GATTGCGGGGACAGACCCCGAGGACCGCGTTCCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGCC 13327
QY 181 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 240
Db 13328 GGGACACCGTCCCTGCCCTTCACTTCAGCTCCGCTCCCTCCGCGGAGCCCGCCCGC 13387
QY 241 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTTCGCGGCGTCCAGAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCGCCAGCCCGCTTCGCGGCGTCCAGAGCCCTCCCTT 13447
QY 301 CCTTTCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 360
Db 13448 CCTTTCGCGCGCGCTCTCTGCGGGCGGAGTTTCAGGAGGAGTGGGGAGTGGTCTGCT 13507
QY 361 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 397
Db 13508 GCGACGTGGGAAGCCCTGGCGCCCGGCGCCACCCCGCG 13544

RESULT 10

US-10-674-836-1
; Sequence 1, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.

```
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/244,438
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-1

Query Match      100.0%; Score 397; DB 17; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCGCTGGCTCCTCGACCTGGAGCGAGCGCGCGCGCGGGGGAAGCGCGGC 60
Db 13148 CCTCGCTGGCTCCTCGACCTGGAGCGAGCGCGCGCGCGGGGGAAGCGCGGC 13207

QY 61 CCAGACCCCGGGTCCGCGGAGCGAGCTGCGCTGTCGGGGCCAGCGCGGGCTCCAGTG 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCGAGCTGCGCTGTCGGGGCCAGCGCGGGCTCCAGTG 13267

QY 121 GATTGCGGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327

QY 181 GGGCACCCGCTGTCGCGCTTACCTTCCAGTCCGCTTCTCCGCGGAGACCCCGCGCG 240
Db 13328 GGGCACCCGCTGTCGCGCTTACCTTCCAGTCCGCTTCTCCGCGGAGACCCCGCGCG 13387

QY 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCGCGCGCTCCCGCTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCGCGCGCTCCCGCTT 13447

QY 301 CTTTTCGGGGCCCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGCAGCGTGGCTCTGCT 360
Db 13448 CTTTTCGGGGCCCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGCAGCGTGGCTCTGCT 13507

QY 361 GGGCAGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
Db 13508 GGGCAGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13544

RESULT 11
US-10-811-012-1
; Sequence 1, Application US/10811012
; Publication No. US20040152189A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: McWhir, Jim
; APPLICANT: Gold, Joseph D.
; APPLICANT: Schiffr, J. Michael
; TITLE OF INVENTION: Selective Antibody Targeting of Undifferentiated Stem Cells
; FILE REFERENCE: 096.006D- Seq18
; CURRENT APPLICATION NUMBER: US/10/811,012
; CURRENT FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: 09/995,419
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 60/253,357
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
```

```
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-811-012-1

Query Match      100.0%; Score 397; DB 18; Length 15418;
Best Local Similarity 100.0%; Pred. No. 5.8e-83;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCGCTGGCTCCTCGACCTGGAGCGAGCGCGCGCGCGGGGGAAGCGCGGC 60
Db 13148 CCTCGCTGGCTCCTCGACCTGGAGCGAGCGCGCGCGCGGGGGAAGCGCGGC 13207

QY 61 CCAGACCCCGGGTCCGCGGAGCGAGCTGCGCTGTCGGGGCCAGCGCGGGCTCCAGTG 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCGAGCTGCGCTGTCGGGGCCAGCGCGGGCTCCAGTG 13267

QY 121 GATTGCGGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 13327

QY 181 GGGCACCCGCTGTCGCGCTTACCTTCCAGTCCGCTTCTCCGCGGAGACCCCGCGCG 240
Db 13328 GGGCACCCGCTGTCGCGCTTACCTTCCAGTCCGCTTCTCCGCGGAGACCCCGCGCG 13387

QY 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCGCGCGCTCCCGCTT 300
Db 13388 TCCGACCCCTCCCGGGTCCCGGCGGAGCGCGCGCGCGCGCGCGCGCTCCCGCTT 13447

QY 301 CTTTTCGGGGCCCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGCAGCGTGGCTCTGCT 360
Db 13448 CTTTTCGGGGCCCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGCAGCGTGGCTCTGCT 13507

QY 361 GGGCAGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
Db 13508 GGGCAGTGGGAAGCCCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 13544

RESULT 12
US-10-840-455-1
; Sequence 1, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-1

Query Match      99.6%; Score 395.4; DB 19; Length 5126;
Best Local Similarity 99.7%; Pred. No. 1.9e-82;
```

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 4727 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 4786

Qy 61 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 4787 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 4846

Qy 121 GATTTCGGGGCACAGACCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 180
Db 4847 GATTTCGGGGCACAGACCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 4906

Qy 181 GGGCACCCGCTCTGCGCCCTTACCTTCCAGCTTCCAGTTCGCGGCGGAGACCGCGCGCG 240
Db 4907 GGGCACCCGCTCTGCGCCCTTACCTTCCAGCTTCCAGTTCGCGGCGGAGACCGCGCGCG 4966

Qy 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 300
Db 4967 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 5026

Qy 301 CCTTTCGCGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 360
Db 5027 CCTTTCGCGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 5086

Qy 361 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 397
Db 5087 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 5123

RESULT 13
US-10-840-455-3
; Sequence 3, Application US/10840455
; Publication No. US2005032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 11276
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-3

Query Match 99.6%; Score 395.4; DB 19; Length 11276;
Best Local Similarity 99.7%; Pred. No. 1.5e-82;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 10877 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 10936

Qy 61 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 10937 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 10996

Qy 121 GATTTCGGGGCACAGACCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 180

Db 10997 GATTTCGGGGCACAGACCCCGAGACCGCGCTCCACAGTGGCGAGGAGCTGGGGACCC 11056

Qy 181 GGGCACCCGCTCTGCGCCCTTACCTTCCAGTTCGCGCTCTCTCGCGGAGACCCCGCGCGC 240
Db 11057 GGGCACCCGCTCTGCGCCCTTACCTTCCAGTTCGCGCTCTCTCGCGGAGACCCCGCGCGC 11116

Qy 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 300
Db 11117 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 11176

Qy 301 CCTTTCGCGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 360
Db 11177 CCTTTCGCGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 11236

Qy 361 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 397
Db 11237 GCGCACGTGGGAAGCCCTTGGCGCCCGCGCACCCCGCG 11273

RESULT 14
US-10-840-455-43
; Sequence 43, Application US/10840455
; Publication No. US2005032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; TITLE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 26414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-43

Query Match 99.6%; Score 395.4; DB 19; Length 26414;
Best Local Similarity 99.7%; Pred. No. 1.2e-82;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 60
Db 10877 CCCTCGTGGCGTCCCTGCACCTTGGAGCGGAGCGCGCGGGGAAAGCGCGC 10936

Qy 61 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 120
Db 10937 CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGTGTGGGGCCAGCGCGGCTCCCAATG 10996

Qy 121 GATTTCGGGGCACAGACCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 180
Db 10997 GATTTCGGGGCACAGACCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 11056

Qy 181 GGGCACCCGCTCTGCGCCCTTACCTTCCAGTTCGCGCTCTCTCGCGGAGACCCCGCGCGC 240
Db 11057 GGGCACCCGCTCTGCGCCCTTACCTTCCAGTTCGCGCTCTCTCGCGGAGACCCCGCGCGC 11116

Qy 241 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 300
Db 11117 TCCGACCCCTCCCGGGTCCCGGCGGAGCCCGCTTCCAGTTCGCGGCGGAGCTGGGGACCC 11176

Qy 301 CCTTTCGCGCGCGCGCGCTCTCTCTCGCGGCGGAGTTTCAGGACGCGCTGCGTCTGCT 360

Db 11177 CTTTTCCGGCGCCCGCCCTCTCTCGGGCGCGAGTTTCAGGCAGCGTGGTCTCTGCT 11236
QY 361 GCGCAGTGGGAGCCCTGGCCCGCCGCGCACCCCGCG 397
Db 11237 GCGCAGTGGGAGCCCTGGCCCGCCGCGCACCCCGCG 11273

RESULT 15
US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Mancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TEST EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
; LOCATION: (25394)...(25549)
; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8

; NAME/KEY: intron
; LOCATION: (31359)...(33943)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
; NAME/KEY: exon
; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
; US-09-733-294A-30

Query Match 99.6%; Score 395.4; DB 9; Length 5152;
Best Local Similarity 99.7%; Pred. No. 9.4e-83;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCCTGCTGGCGTCCCTGCAACCCCTGGAGCGGCGCGCGGGGGAAGCGCGC 60
Db 10877 CCCTGCTGGCGTCCCTGCAACCCCTGGAGCGGCGCGCGGGGGAAGCGCGC 10936
QY 61 CCAGACCCCGGGTCCGCGCCCGAGAGAGCTGCGCTGTCTGGGGCCAGCGCGGGTCTCCAGTG 120
Db 10937 CCAGACCCCGGGTCCGCGCCCGAGAGAGCTGCGCTGTCTGGGGCCAGCGCGGGTCTCCAGTG 10996
QY 121 GATTCCGGGGCA CAGACGCCCAAGACCGCGCTTCCCACTGCGGGAGGACTGGGGACCC 180
Db 10997 GATTCCGGGGCA CAGACGCCCAAGACCGCGCTTCCCACTGCGGGAGGACTGGGGACCC 11056
QY 181 GGGCACCCGCTCTGCGCCCTTCCAGCTCCGCTCTCTCCGCGCGGACCCCGGCCCG 240
Db 11057 GGGCACCCGCTCTGCGCCCTTCCAGCTCTCTCCGCGCGGACCCCGGCCCG 11116


```

Qy      241  TCCGACCCCTCCCGGTCCCGGCCAGCCCCCTCCGGGCCCTCCAGCCCTCCCTT 300
Db      11117 TCCGACCCCTCCCGGTCCCGGCCAGCCCCCTCCGGGCCCTCCAGCCCTCCCTT 11176

Qy      301  CCTTTCGGCGCCCGCCCTCTCCTCGCGGCCGAGTTTCAGGCAAGCGTGGTCTCTGCT 360
Db      11177 CCTTTCGGCGCCCGCCCTCTCCTCGCGGCCGAGTTTCAGGCAAGCGTGGTCTCTGCT 11236

Qy      361  GCGCACGTGGGAAGCCCTGGGCCCGGCCACCCCGCG 397
Db      11237 GCGCACGTGGGAAGCCCTGGGCCCGGCCACCCCGCG 11273

```

Search completed: April 9, 2005, 10:41:30
 Job time : 510.69 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:45:13 ; Search time 126.15 Seconds
(without alignments)
5149.459 Million cell updates/sec

Title: US-10-081-969-93

Perfect score: 397
Sequence: 1 cccctcggtggcctcgtca.....tggcccccggccaccacccgcg 397

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818130359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	4321	4	US-09-402-181B-6
2	397	100.0	15418	4	US-09-783-203-1
3	397	100.0	15418	4	US-09-804-427A-1
4	397	100.0	15418	4	US-09-244-438-1
5	395.4	99.6	44952	4	US-09-949-016-12197
6	395.4	99.6	44960	4	US-09-949-016-17583
7	395.4	99.6	51552	4	US-09-733-294A-30
8	354.2	89.2	35871	4	US-09-956-335-2
9	354.2	89.2	35978	4	US-09-956-335-1
10	351	88.4	1677	4	US-09-956-335-3
11	341.8	86.1	4335	3	US-08-974-549A-6
12	341.8	86.1	4335	4	US-09-721-456-6
13	338.8	85.3	4200	4	US-08-912-951-6
14	298.2	75.1	314	4	US-09-916-510A-8
15	295	74.3	298	4	US-09-244-438-17
16	256.4	64.6	261	4	US-09-932-581-24
17	256.4	64.6	5928	4	US-09-932-581-25
18	93.6	23.6	124	3	US-08-974-549A-726
19	93.6	23.6	124	4	US-09-721-456-726
20	77	13.4	78	4	US-09-932-581-7
21	74	18.6	77	4	US-09-244-438-19
22	74	18.6	89	4	US-09-244-438-20
23	65.2	16.4	319	3	US-09-165-264-8
24	64.6	16.3	320	3	US-09-165-264-7
25	64	16.1	865	4	US-09-270-767-11042
26	63.2	15.9	320	3	US-09-165-264-14
27	62.2	15.7	320	3	US-09-165-264-13

C 28	62.2	15.7	14340	4	US-09-949-016-16972	Sequence 16972, A
C 29	62	15.6	318	3	US-09-165-264-12	Sequence 12, Appl
C 30	61.8	15.6	54779	4	US-09-949-001-27	Sequence 27, Appl
C 31	61.8	15.6	54780	4	US-09-949-001-39	Sequence 39, Appl
C 32	61.2	15.4	320	3	US-09-165-264-11	Sequence 11, Appl
C 33	60.2	15.2	8100	4	US-09-949-016-13460	Sequence 13460, A
C 34	60.2	15.2	8100	4	US-09-949-016-13461	Sequence 13461, A
C 35	58.6	14.8	7218	1	US-08-232-463-14	Sequence 14, Appl
C 36	58.2	14.7	393	4	US-09-107-433-1828	Sequence 1828, Ap
C 37	58.2	14.7	690	4	US-09-107-433-226	Sequence 226, App
C 38	58.2	14.7	795	4	US-09-107-433-195	Sequence 195, App
C 39	58.2	14.7	1536	4	US-09-107-433-301	Sequence 301, App
C 40	58.2	14.7	152331	3	US-09-128-155-16	Sequence 16, Appl
C 41	57.8	14.6	2561	4	US-09-616-289-48	Sequence 48, Appl
C 42	57.6	14.5	2376	4	US-09-023-655-932	Sequence 932, App
C 43	57.6	14.5	2404	3	US-08-945-771-1	Sequence 1, Appl
C 44	57.2	14.4	12001	1	US-08-458-568A-11	Sequence 11, Appl
C 45	57.2	14.4	670689	4	US-09-949-016-12505	Sequence 12505, A

ALIGNMENTS

RESULT 1

US-09-402-181B-6
; Sequence 6, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:

Qy 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 13267
Qy 121 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 13227
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCGCGCCG 240
Db 13328 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCGCGCCG 13387
Qy 241 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 13447
Qy 301 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 360
Db 13448 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGCGCCCGCGCCAGCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGCGCCCGCGCCAGCCCGCG 13544
RESULT 4
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244, 438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1
Query Match 100.0%; Score 397; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 3.2e-71;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGGCTCCCTGCACCTTGGAGCGAGCGCGCGGGGAGGAGCGCGC 60
Db 13148 CCCTCGCTGGGCTCCCTGCACCTTGGAGCGAGCGCGCGGGGAGGAGCGCGC 13207
Qy 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 13208 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 13267
Qy 121 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCGCGCCG 240
Db 13328 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCGCGCCG 13387
Qy 241 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 300
Db 13388 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 13447
Qy 301 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 360
Db 13448 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGCGCCCGCGCCAGCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGCGCCCGCGCCAGCCCGCG 13544

Db 13388 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGGACCCCTTCCCTT 13447
Qy 301 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 360
Db 13448 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTTGGCCCGCGGACCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTTGGCCCGCGGACCCCGCG 13544
RESULT 5
US-09-949-016-12197
; Sequence 12197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197
Query Match 99.6%; Score 395.4; DB 4; Length 44952;
Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGGCTCCCTGCACCTTGGAGCGCGCGCGCGCGGGAAGCGCGC 60
Db 1659 CCCTCGCTGGGCTCCCTGCACCTTGGAGCGCGCGCGCGCGGGAAGCGCGC 1718
Qy 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 120
Db 1719 CCAGACCCCGGGTCCGCGGAGCAGCTGCGTGTGCGGGCCAGGCGCGGCTCCCAAGT 1778
Qy 121 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db 1779 GATTGCGGGGCACAGACCCGAGGACCGCTTCCACGTGGCGGAGGACTGGGGACCC 1838
Qy 181 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCCGCGC 240
Db 1839 GGGACACCGTCTGCGCCCTTCCACCTTCCAGCTGCGCTTCTCCGCGGCGGACCCCGCGC 1898
Qy 241 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 300
Db 1899 TCCGACCCCTCCGCGGTCCGCGCCAGCCCTTCCGCGGCTTCCAGCCCTCCCTT 1958
Qy 301 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 360
Db 1959 CCTTTCGCGGCGCGCCCTTCTCTCGCGGCGGAGTTTTCAGGACGCGCTCGCTCCTGCT 2018
Qy 361 GCGCAGCTGGGAAGCCCTTGGCCCGCGGACCCCGCG 397
Db 2019 GCGCAGCTGGGAAGCCCTTGGCCCGCGGACCCCGCG 2055

NAME/KEY: exon
LOCATION: (37885)...(38073)
OTHER INFORMATION: exon 11
NAME/KEY: intron
LOCATION: (38074)...(41874)
OTHER INFORMATION: intron 11
NAME/KEY: exon
LOCATION: (41875)...(42001)
OTHER INFORMATION: exon 12
NAME/KEY: intron
LOCATION: (42002)...(42881)
OTHER INFORMATION: intron 12
NAME/KEY: exon
LOCATION: (42882)...(42943)
OTHER INFORMATION: exon 13
NAME/KEY: intron
LOCATION: (42944)...(46129)
OTHER INFORMATION: intron 13
NAME/KEY: exon
LOCATION: (46130)...(46254)
OTHER INFORMATION: exon 14
NAME/KEY: intron
LOCATION: (46255)...(47035)
OTHER INFORMATION: intron 14
NAME/KEY: exon
LOCATION: (47036)...(47173)
OTHER INFORMATION: exon 15
NAME/KEY: intron
LOCATION: (47174)...(47709)
OTHER INFORMATION: intron 15
NAME/KEY: exon
LOCATION: (47710)...(50544)
OTHER INFORMATION: exon 16
US-09-733-294A-30

Query Match 99.6%; Score 395.4; DB 4; Length 51552;

Best Local Similarity 99.7%; Pred. No. 6.8e-71;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCTCGTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGC 60
DB 10877 CCCTCGTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGC 10936

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGCGCGGGCTCCCACTG 120
DB 10937 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGCGCGGGCTCCCACTG 10996

QY 121 GATTCGGGGCACAGACGCCCGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
DB 10997 GATTCGGGGCACAGACGCCCGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 11056

QY 181 GGGCACCGCTCTGCGCCCTTACCTTCCAGCTCCGCTTCCGCGGAGCCCGCGCCCG 240
DB 11057 GGGCACCGCTCTGCGCCCTTACCTTCCAGCTCCGCTTCCGCGGAGCCCGCGCCCG 11116

QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCCCTTCCGCGGCTCCAGCCCTCCCTT 300
DB 11117 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCCCTTCCGCGGCTCCAGCCCTCCCTT 11176

QY 301 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTGGCTCTGCT 360
DB 11177 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTGGCTCTGCT 11236

QY 361 GCGCAGTGGGAAGCCCTGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 397
DB 11237 GCGCAGTGGGAAGCCCTGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11273

RESULT 8

US-09-956-335-2/c
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:

APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: KUPPASWAMI, Mohan
APPLICANT: DORONIN, Konsantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956.335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 35871
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-2

Query Match 89.2%; Score 354.2; DB 4; Length 35871;

Best Local Similarity 99.2%; Pred. No. 1.2e-62;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTCGTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGC 60
DB 34385 CCCTCGTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGC 34326

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGCGCGGGCTCCCACTG 120
DB 34325 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTGCGGGCCAGCGCGGGCTCCCACTG 34266

QY 121 GATTCGGGGCACAGACGCCCGGAGCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
DB 34265 GATTCGGGGCACAGACGCCCGGAGCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 34206

QY 181 GGGCACCGCTCTGCGCCCTTCCAGCTCCGCTTCCGCGGAGCCCGCGGCGGCGGCGG 240
DB 34205 GGGCACCGCTCTGCGCCCTTCCAGCTCCGCTTCCGCGGAGCCCGCGGCGGCGGCGG 34146

QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCCCTTCCGCGGCTCCAGCCCTCCCTT 300
DB 34145 TCCGACCCCTCCCGGGTCCCGCGGAGCAGCCCTTCCGCGGCTCCAGCCCTCCCTT 34086

QY 301 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTGGCTCTGTC 359
DB 34085 CCTTTCCGGGCGCGCGCTCTCTCTGCGGGCGGAGTTTCAGGACGCGTGGCTCTGTC 34027

RESULT 9

US-09-956-335-1/c
; Sequence 1, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:

APPLICANT: WOLD, William
APPLICANT: TOTH, Karoly
APPLICANT: KUPPASWAMI, Mohan
APPLICANT: DORONIN, Konsantin
TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
FILE REFERENCE: 16153-8394
CURRENT APPLICATION NUMBER: US/09/956.335
CURRENT FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 35978
TYPE: DNA
ORGANISM: Adenovirus
US-09-956-335-1

Query Match 89.2%; Score 354.2; DB 4; Length 35978;

Best Local Similarity 99.2%; Pred. No. 1.2e-62;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCTCGTGGGCTCCCTGCACCTGGGAGCGGAGCGCGCGGGCGGGAAGCGCGC 60


```
Db 34492 CCCTCGTGGCTCCCTGACCTGGAGCGAGCGCGCGCGGGAAGCGCGGC 34433
Qy 61 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGGGGCAGGCGGGCTCCAGTG 120
Db 34432 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGGGGCAGGCGGGCTCCAGTG 34373
Qy 121 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACACTGCGGAGGACTGGGAGCC 180
Db 34372 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACACTGCGGAGGACTGGGAGCC 34313
Qy 181 GGGACACCGTCTGCGCCCTTACCTTCCAGCTTCCGCTCTCCGCGGAGACCCGCGCG 240
Db 34312 GGGACACCGTCTGCGCCCTTACCTTCCAGCTTCCGCTCTCCGCGGAGACCCGCGCG 34253
Qy 241 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 34252 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 34193
Qy 301 CCTTTCCGCGCGCGCGCGCTCTCTCGCGGCGGAGTTTCAGGACGCGTGGTCTGC 359
Db 34192 CCTTTCCGCGCGCGCGCGCTCTCTCGCGGCGGAGTTTCAGGACGCGTGGTCTGC 34134
```

RESULT 10

US-09-956-335-3/c
; Sequence 3, Application US/09956335
; Patent No. 6627190

; GENERAL INFORMATION:
; APPLICANT: WOLD, William

; APPLICANT: TOTTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan

; APPLICANT: DORONIN, Konsantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE

; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394

; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3
; LENGTH: 1677

; TYPE: DNA
; ORGANISM: Adenovirus

US-09-956-335-3

Query Match 88.4%; Score 351; DB 4; Length 1677;

Best Local Similarity 100.0%; Pred. No. 5.2e-62; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0;

```
Qy 1 CCCTCGTGGCTCCCTGACCTGGAGCGGAGCGGCGCGGCGGCGGGAAGCGCGGC 60
Db 353 CCCTCGTGGCTCCCTGACCTGGAGCGGAGCGGCGGCGGCGGGAAGCGCGGC 294
Qy 61 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGGGGCAGGCGGGCTCCAGTG 120
Db 293 CCAGACCCCGCGGTCGCGCCGAGAGCTGCGCTGTCGGGGCAGGCGGGCTCCAGTG 234
Qy 121 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACACTGCGGAGGACTGGGAGCC 180
Db 233 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACACTGCGGAGGACTGGGAGCC 174
Qy 181 GGGACACCGTCTGCGCCCTTACCTTCCAGCTCCGCTCTCCGCGGAGACCCGCGCG 240
Db 173 GGGACACCGTCTGCGCCCTTACCTTCCAGCTCCGCTCTCCGCGGAGACCCGCGCG 114
Qy 241 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 113 TCCCGACCCCTCCCGGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 54
Qy 301 CCTTTCCGCGCGCGCGCGCTCTCTCGCGGCGGAGTTTCAGGACGCGTG 351
Db 53 CCTTTCCGCGCGCGCGCGCTCTCTCGCGGCGGAGTTTCAGGACGCGTG 3
```

RESULT 11

US-08-974-549A-6

; Sequence 6, Application US/08974549A
; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cecch, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 4335 base pairs

; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
; US-08-974-549A-6

Query Match      86.1%; Score 341.8; DB 3; Length 4335;
Best Local Similarity 97.3%; Pred. No. 3.7e-60;
Matches 390; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

Qy 1 CCCTCGCTGGGTCCTCGACCTGGGAGCGGAGCGGCGCGGGGGAAGCGCGGC 60
Db 2095 CCCTCGCTGGGTCCTCGACCTGGGAGCGGAGCGGCGCGGGCGGGAAGCGCGGC 2154

Qy 61 CCAGACCCCGGTCGCGCCCGGAGCAGCTGCGCTGTGCGGCGCCAGCGCGGCTCCAGTG 120
Db 2155 CCAGACCCCGGTCGCGCCCGGAGCAGCTGCGCTGTGCGGCGCCAGCGCGGCTCCAGTG 2214

Qy 121 GATTGCGGGC-ACAGACGCCAGGACCGCGCTTCCACGTCGCGGAGGACTGGGACC 179
Db 2215 GATTGCGGGC-ACAGACGCCAGGACCGCGCTTCCACGTCGCGGAGGACTGGGACC 2274

Qy 180 CGGACACCGCTCTGCGCCCTTCCACCTTCCAGTCGCGCTCTGCGCGGG-ACCCGCGCC 238
Db 2275 CGGACACCGCTCTGCGCCCTTCCACCTTCCAGTCGCGCTCTGCGCGGGAGACCCGCGCC 2334

Qy 239 GTCCTCG-ACCCCTTCCGGTCCCGCCGCGGAGCGGCGGCGGCTCCAGCGGCTCC 297
Db 2335 GTCCTCG-ACCCCTTCCGGTCCCGCCGCGGAGCGGCGGCGGCTCCAGCGGCTCC 2394

Qy 298 CTTCC-TTTCGCGGCGCGGCTCTCTCGGCGGCGGAGTTTCAAGCAGCGCTGCTCC 356
Db 2395 GTTCTTTTCGCGGCGCGGCTCTCTCGGCGGCGGAGTTTCAAGCAGCGCTGCTCC 2454

Qy 357 TGCTGCGCAGCTGGGAAGCCTTGCGCCCGGCGGACCCCGCG 397
Db 2455 TGCTGCGCAGCTGGGAAGCCTTGCGCCCGGCGGACCCCGCG 2495

RESULT 12
US-09-721-456-6
; Sequence 6, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;               Lingner, Joachim
;               Nakamura, Toru
;               Chapman, Karen B.
;               Morin, Gregg B.
;               Harley, Calvin B.
;               Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721.456
; FILING DATE: 22-Nov. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974.549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724.643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844.419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846.017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851.843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854.050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911.312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912.951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915.503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4335
; OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2715..2818
; OTHER INFORMATION: /note= "intron 1"
; FEATURE:
; NAME/KEY: intron
; LOCATION: 4173..4326
; OTHER INFORMATION: /note= "intron 2"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-721-456-6

Query Match      86.1%; Score 341.8; DB 4; Length 4335;
Best Local Similarity 97.3%; Pred. No. 3.7e-60;
Matches 390; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

Qy 1 CCCTCGCTGGGTCCTCGACCTGGGAGCGGAGCGGCGCGGGGGAAGCGCGGC 60
Db 2095 CCCTCGCTGGGTCCTCGACCTGGGAGCGGAGCGGCGCGGGCGGGAAGCGCGGC 2154

Qy 61 CCAGACCCCGGTCGCGCCCGGAGCAGCTGCGCTGTGCGGCGCCAGCGCGGCTCCAGTG 120
Db 2155 CCAGACCCCGGTCGCGCCCGGAGCAGCTGCGCTGTGCGGCGCCAGCGCGGCTCCAGTG 2214

Qy 121 GATTGCGGGC-ACAGACGCCAGGACCGCGCTTCCACGTCGCGGAGGACTGGGACC 179
Db 2215 GATTGCGGGC-ACAGACGCCAGGACCGCGCTTCCACGTCGCGGAGGACTGGGACC 2274

Qy 180 CGGACACCGCTCTGCGCCCTTCCACCTTCCAGTCGCGCTCTGCGCGGG-ACCCGCGCC 238
Db 2275 CGGACACCGCTCTGCGCCCTTCCACCTTCCAGTCGCGCTCTGCGCGGGAGACCCGCGCC 2334

Qy 239 GTCCTCG-ACCCCTTCCGGTCCCGCCGCGGAGCGGCGGCGGCTCCAGCGGCTCC 297
Db 2335 GTCCTCG-ACCCCTTCCGGTCCCGCCGCGGAGCGGCGGCGGCTCCAGCGGCTCC 2394

Qy 298 CTTCC-TTTCGCGGCGCGGCTCTCTCGGCGGCGGAGTTTCAAGCAGCGCTGCTCC 356
Db 2395 GTTCTTTTCGCGGCGCGGCTCTCTCGGCGGCGGAGTTTCAAGCAGCGCTGCTCC 2454

Qy 357 TGCTGCGCAGCTGGGAAGCCTTGCGCCCGGCGGACCCCGCG 397
Db 2455 TGCTGCGCAGCTGGGAAGCCTTGCGCCCGGCGGACCCCGCG 2495

```


Search completed: April 9, 2005, 07:05:39
Job time : 130.15 secs

```
Db 1 AGCAGCTGGCTGTCGGGGCCAGGCGGGCTCCCACTGGATTCTGGGGGACAGAGCCCA 60
QY 143 GGACCGCGTTCCCACTGGGGGAGGAGCTGGGGACCGGGGACCCGTCCTGCCCCCTTCA 202
Db 61 GGACCGCGTTCCCACTGGGGGAGGAGCTGGGGACCGGGGACCCGTCCTGCCCCCTTCA 120
QY 203 CTTTCCAGTCCGCTCCTCGCGGGGACCCCGGCCCGTCCGACCCCTCGGGGTCCCC 262
Db 121 CTTTCCAGTCCGCTCCTCGCGGGGACCCCGGCCCGTCCGACCCCTCGGGGTCCCC 180
QY 263 GGCCAGACCCCTCCGGGCGCTTCCAGGCCCTTCCCTTCCGCGCGCCCGGCCCTCT 322
Db 181 GGCCAGACCCCTCCGGGCGCTTCCAGGCCCTTCCCTTCCGCGCGCCCGGCCCTCT 239
QY 323 CTTCCGGGCGGAGTTTTCAGGAGCGCTGCGTCTGTCGCACTGGGAAAGCCCTGGCC 382
Db 240 CTTCCGGGCGGAGTTTTCAGGAGCGCTGCGTCTGTCGCACTGGGAAAGCCCTGGCC 299
QY 383 CCGGCACCCCGCG 397
Db 300 CCGGCACCCCGCG 314
```

RESULT 15

US-09-244-438-17

; Sequence 17, Application US/09244438

; Patent No. 6777203

; GENERAL INFORMATION:

; APPLICANT: Morin, Gregg B.

; APPLICANT: Lichtsteiner, Serge

; APPLICANT: Vasserot, Alain

; APPLICANT: Adams, Robert R.

; APPLICANT: Geron Corporation

; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional

; FILE OF INVENTION: Regulatory Sequences and Methods of Using

; FILE REFERENCE: 019/246P

; CURRENT APPLICATION NUMBER: US/09/244,438

; CURRENT FILING DATE: 1999-02-04

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 298

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Human TERT promoter

US-09-244-438-17

Query Match

Best Local Similarity 74.3%; Score 295; DB 4; Length 298;

Matches 295; Conservativeness 100.0%; Pred. No. 8.7e-51;

Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 103 CAGGCGGGCTCCCACTGGATTTCGGGGGACAGAGCCCGGCGCTTCCCACTGG 162
Db 1 CAGGCGGGCTCCCACTGGATTTCGGGGGACAGAGCCCGGCGCTTCCCACTGG 60
QY 163 CGGAGGAGTGGGACCGGGGACCCGCTCCTGCGGCTTCCAGCTCGGCTCCTC 222
Db 61 CGGAGGAGTGGGACCGGGGACCCGCTCCTGCGGCTTCCAGCTCGGCTCCTC 120
QY 223 CGGCGGACCGGCGCCCGTCCGACCCCTTCGGGTCCCGGCCAGCCCGCTCCGGGCC 282
Db 121 CGGCGGACCGGCGCCCGTCCGACCCCTTCGGGTCCCGGCCAGCCCGCTCCGGGCC 180
QY 283 CTCCGAGCCCTCCGCTTCTTCCGCGGCGCCCGGCTTCTCTCGGGGGAGTTTCA 342
Db 181 CTCCGAGCCCTCCGCTTCTTCCGCGGCGCCCGGCTTCTCTCGGGGGAGTTTCA 240
QY 343 GCAGGCTGCGTCTGCTGCGGAGCCCTTGGGAGCCCTTGGCCCGGCGCCCGGCG 397
Db 241 GCAGGCTGCGTCTGCTGCGGAGCCCTTGGGAGCCCTTGGCCCGGCGCCCGGCG 295
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 04:29:03 ; Search time 416.17 Seconds
(without alignment)
5647.064 Million cell updates/sec

Title: US-10-081-969-93

Perfect score: 397
Sequence: 1 cccctgctggcctcctgca.....tggccccggccaccctccgcg 397

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_16Dec04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001as:*
 - 5: Geneseq2001bs:*
 - 6: Geneseq2002as:*
 - 7: Geneseq2002bs:*
 - 8: Geneseq2003as:*
 - 9: Geneseq2003bs:*
 - 10: Geneseq2003cs:*
 - 11: Geneseq2003ds:*
 - 12: Geneseq2004as:*
 - 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	397	100.0	397	6	ABs98658 Human TER
2	397	100.0	408	13	Adr73423 Human tel
3	397	100.0	902	13	Adr73427 Human m-h
4	397	100.0	3962	4	Aah41091 Telomerase
5	397	100.0	15418	3	Aas63785 Nucleotid
6	397	100.0	15418	6	Aal38601 Human TER
7	397	100.0	15418	6	ABs54997 Lambda cl
8	397	100.0	15418	6	ABs54997 Lambda cl
9	397	100.0	15418	10	Adc21253 Lambda cl
10	395.4	99.6	455	12	Adi33422 Human tel
11	395.4	99.6	5126	2	Aax88272 Human cat
12	395.4	99.6	51552	6	Aas96607 DNA encod
13	376.4	94.8	378	8	Acc47272 CEA gene
c 14	354.2	89.2	35871	6	Ad27972 Recombina
c 15	354.2	89.2	35978	6	Ad27971 Recombina
c 16	351	88.4	1677	6	Ad27973 Human tel
17	341.8	86.1	4335	2	Aav16979 Human tel
18	328.6	82.8	454	11	Adn00285 Tumour-sp
19	298.2	75.1	314	3	Aaa94134 Telomerase
c 20	273.8	69.0	4356	6	ABU92335 Chemicall

21	260.4	65.6	327	6	AAL55438	Aal55438 Specific
22	260.4	65.6	327	12	ADI80429	Adi80429 Anti-tumo
23	259	65.2	293	6	AAL55435	Aal55435 Specific
24	259	65.2	293	6	ABQ76069	Abq76069 Anticance
25	256.4	64.6	261	6	ABK12706	Abk12706 Human tel
26	256.4	64.6	295	8	ABV75307	Abv75307 Telomerase
27	256.4	64.6	295	8	ABV75306	Abv75306 TERT mini
28	256.4	64.6	295	10	ABZ23897	Abz23897 TERT mini
29	256.4	64.6	5928	6	ABK12707	Abk12707 Minimal t
30	244	61.5	245	6	ABs98659	AbS98659 Human TER
c 31	244	61.5	955	6	ABs98580	AbS98580 Ar17pAE2f
32	216.4	54.5	240	10	ABZ23898	Abz23898 Telomerase
c 33	212.2	53.5	1404	6	AAD22344	Aad22344 Chemicall
c 34	199.8	50.3	403	6	ABs98583	AbS98583 Ar17pAE2f
35	181.2	45.6	4356	6	ABL92334	AbL92334 Chemicall
36	144	36.3	144	8	ABZ79850	AbZ79850 TERT mini
37	133.6	33.7	1404	6	AAD22343	Aad22343 Chemicall
38	88	22.2	89	6	ABV73905	Abv73905 Telomerase
39	77	19.4	78	6	ABV74896	Abv74896 Minimal t
40	77	19.4	78	6	ABZ79851	AbZ79851 Human elt
41	77	19.4	78	10	ABZ22591	AbZ22591 Human TER
c 42	70.6	17.8	3163	10	ADC87060	AdC87060 Human GPC
c 43	68.6	17.3	629	13	ACN54594	ACN54594 Cotton an
c 44	68.2	17.2	3133	10	ADC86738	AdC86738 Human GPC
c 45	67.8	17.1	588	13	ACN54596	ACN54596 Cotton an

ALIGNMENTS

RESULT 1

ABs98658
ID ABs98658 standard; DNA; 397 BP.

AC ABs98658;

DT 17-DEC-2002 (first entry)

DE Human TERT promoter sequence #1.

KW Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
KW inverted terminal repeat; ITR; termination signal sequence; lung cancer;
KW E2F responsive promoter; adenoviral packaging signal; prostate cancer;
KW neoplastic condition; colon cancer; cytostatic; immunostimulant;
KW gene therapy; human; TERT; promoter; ds.

OS Homo sapiens

PN 02000267861-A2

XX

PD 06-SEP-2002.

PF 22-FEB-2002; 2002WO-US005300.

XX 23-FEB-2001; 2001US-0270922P.

PR 01-JUN-2001; 2001US-0295037P.

XX 14-JAN-2002; 2002US-0348670P.

PA (NOVS) NOVARTIS PHARMA AG.

XX Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CW;

PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;

PI Police SR, Clarke L, Phipps S, Cheng C;

XX WPI; 2002-706950/76.

XX Recombinant viral vector comprising an adenoviral nucleic acid backbone,
PT useful for treating neoplastic disorders such as lung, breast, prostate
or colon cancer.

XX Claim 11; Page 21; 226pp; English.

CC The present invention relates to a new recombinant viral vector

```
CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX
SQ Sequence 397 BP; 35 A; 186 C; 127 G; 49 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 6; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGCGTCCCTGCACACCTGGAGCGCGAGCGCGCGCGGGAAGCGCGC 60
DB 1 CCCTCGCTGGCGTCCCTGCACACCTGGAGCGCGAGCGCGCGCGGGAAGCGCGC 60
QY 61 CCAGACCCCGGGTCCGCGCGAGAGCTGCGCTGTTCGGGGCCAGGCCCGGGTCCCAAGT 120
DB 61 CCAGACCCCGGGTCCGCGCGAGAGCTGCGCTGTTCGGGGCCAGGCCCGGGTCCCAAGT 120
QY 121 GATTTCGGGGCACAGACGCCCGAGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
DB 121 GATTTCGGGGCACAGACGCCCGAGACCGCGCTTCCACAGTGGCGGAGGACTGGGGACCC 180
QY 181 GGGCACCCGCTCTGCGGCTTTCACCTTCAGCTCCGCTCTCCGCGCGACCCCGCGCG 240
DB 181 GGGCACCCGCTCTGCGGCTTTCACCTTCAGCTCCGCTCTCCGCGCGAGACCCCGCGCG 240
QY 241 TCCGACCCCTCCGGGTCCCGGCGGAGCGCCCTTCGGGGCCCTCCAGCCCTCCCTT 300
DB 241 TCCGACCCCTCCGGGTCCCGGCGGAGCGCCCTTCGGGGCCCTTCAGCCCTCCCTT 300
QY 301 CCTTTTCGGCGGCGCGGCTCTCTCGCGCGGAGTTTCAGGACGCGTTCGCTCTGCT 360
DB 301 CCTTTTCGGCGGCGCGGCTCTCTCGCGCGGAGTTTCAGGACGCGTTCGCTCTGCT 360
QY 361 GCGCACGTGGGAGCGCTTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
DB 361 GCGCACGTGGGAGCGCTTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
RESULT 2
ADR73423
ID ADR73423 standard; DNA; 408 BP.
XX
AC ADR73423;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomerase reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; SPl binding site; Cancer.
XX
OS Homo sapiens.
XX
PN WO2004076668-A1.
XX
PD 10-SEP-2004.
XX
PF 27-FEB-2004; 2004WO-KR000427.
XX
PR 27-FEB-2003; 2003KR-00012364.
XX
PA (YUNC/) YUN C.
PA (KIMJ/) KIM J.
XX
```

```
PI Yun C, Kim J, Yang J;
XX
DR WPI; 2004-653423/63.
XX
PT New transcriptional regulatory sequence with a human telomere reverse
PT transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
PT ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
PT head and neck cancer.
XX
PS Disclosure; SEQ ID NO 1; 130pp; English.
XX
CC The invention relates to a transcriptional regulatory sequence with a
CC human telomere reverse transcriptase (hTERT) promoter linked to a
CC nucleotide sequence comprising one or more c-Myc binding sites and/or one
CC or more SPl binding sites. The transcriptional regulatory sequence and
CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
CC colon, cervical, breast, brain, or head and neck cancer. This sequence
CC corresponds to the wild type human telomerase reverse transcriptase
CC (hTERT) promoter sequence used to generate the novel sequence of the
CC invention.
XX
SQ Sequence 408 BP; 35 A; 190 C; 132 G; 51 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 13; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.9e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGGTCCCTGCACCCCTGGAGCGCGAGCGCGCGGGAAGCGCGC 60
DB 12 CCCTCGCTGGGTCCCTGCACCCCTGGAGCGCGAGCGCGCGGGAAGCGCGC 71
QY 61 CCAGACCCCGGGTCCGCGCGAGAGCTGCGCTGTTCGGGGCCAGGCCCGGGTCCCAAGT 120
DB 72 CCAGACCCCGGGTCCGCGCGAGAGCTGCGCTGTTCGGGGCCAGGCCCGGGTCCCAAGT 131
QY 121 GATTTCGGGGCACAGACGCCCGAGCGCTTCCACAGTTCGCGGGCCAGGCCCGGGTCCCAAGT 180
DB 132 GATTTCGGGGCACAGACGCCCGAGCGCGCTTCCACAGTTCGCGGGAGGACTGGGGACCC 191
QY 181 GGGCACCCGCTCTGCGGCTTTCACCTTCAGCTTCGCGCGCGAGCGCGCGCGCGCG 240
DB 192 GGGCACCCGCTCTGCGGCTTTCACCTTCAGCTTCGCGCGCGAGCGCGCGCGCGCG 251
QY 241 TCCGACCCCTCCGGGTCCCGGCGGAGCGCCCTTCGGGGCCCTTCAGCCCTCCCTT 300
DB 252 TCCGACCCCTCCGGGTCCCGGCGGAGCGCCCTTCGGGGCCCTTCAGCCCTCCCTT 311
QY 301 CCTTTTCGGCGGCGCGGCTCTCTCGCGCGGAGTTTCAGGACGCGTTCGCTCTGCT 360
DB 312 CCTTTTCGGCGGCGCGGCTCTCTCGCGCGGAGTTTCAGGACGCGTTCGCTCTGCT 371
QY 361 GGGCACGTGGGAGCGCTTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 397
DB 372 GGGCACGTGGGAGCGCTTCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 408
RESULT 3
ADR73427
ID ADR73427 standard; DNA; 902 BP.
XX
AC ADR73427;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human m-hTERT gene promoter sequence.
XX
KW ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomerase reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; SPl binding site; cancer.
XX
OS Homo sapiens.
XX
```


PH Key Location/Qualifiers
 FT protein_bind 173..178 /tag= a
 FT protein_bind /bound_moiety= "c-Myc protein"
 FT protein_bind 228..236 /tag= b
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 250..255 /tag= c
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 282..290 /tag= d
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 302..310 /tag= e
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 331..336 /tag= f
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 381..386 /tag= g
 FT protein_bind /bound_moiety= "c-Myc protein"
 FT protein_bind 617..622 /tag= h
 FT protein_bind /bound_moiety= "c-Myc protein"
 FT protein_bind 672..680 /tag= i
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 694..699 /tag= j
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 726..734 /tag= k
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 746..754 /tag= l
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT protein_bind 775..780 /tag= m
 FT protein_bind /bound_moiety= "Spl transcription factor"
 FT misc_feature 900 /tag= n
 FT /note= "translation start site"
 PN WO2004076668-A1.
 XX 10-SEP-2004.
 XX 27-FEB-2004; 2004WO-KR000427.
 XX 27-FEB-2003; 2003KR-00012364.
 XX (YUNC/) YUN C.
 XX (KIMJ/) KIM J.
 XX Yun C, Kim J, Yang J;
 XX WPI; 2004-653423/63.
 XX New transcriptional regulatory sequence with a human telomere reverse
 PT transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
 PT ovarian, liver, pancreatic, bladder, colon, cervical, breast, or
 PT head and neck cancer.
 XX Claim 6; SEQ ID NO 13; 130pp; English.
 XX The invention relates to a transcriptional regulatory sequence with a
 CC human telomere reverse transcriptase (hTERT) promoter linked to a
 CC nucleotide sequence comprising one or more c-Myc binding sites and/or one
 CC or more Spl binding sites. The transcriptional regulatory sequence and
 CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
 CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
 CC colon, cervical, breast, brain, or head and neck cancer. This sequence

CC corresponds to the modified human telomerase reverse transcriptase
 CC (hTERT) promoter sequence containing the extra c-Myc and Spl binding site
 CC sequences.
 XX Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 397; DB 13; Length 902;
 Best Local Similarity 100.0%; Pred. No. 2.5e-56;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGCGCGCGCGGGAAGCGCGC 60
 DB 18 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGCGCGCGCGGGAAGCGCGC 77
 QY 61 CCAGACCCCGGGTCCCGCCCGGAGCAGCTGCGTGTGCGGGCCAGGCGGGCTCCCATG 120
 DB 78 CCAGACCCCGGGTCCCGCCCGGAGCAGCTGCGTGTGCGGGCCAGGCGGGCTCCCATG 137
 QY 121 GATTGGGGGACAGAGCCCGCGCTCCACGTGGCGGAGGAGCTGGGGACCC 180
 DB 138 GATTGGGGGACAGAGCCCGCGCTCCACGTGGCGGAGGAGCTGGGGACCC 197
 QY 181 GGGCACCGCTCTGCCCTTCCACCTTCAGCTCCGCTCCCTCCGCGCGACCCCGCCCG 240
 DB 198 GGGCACCGCTCTGCCCTTCCACCTTCAGCTCCGCTCCCTCCGCGCGACCCCGCCCG 257
 QY 241 TCCGACCCCTCCCGGGTCCCGCCCGGAGCAGCCCTCCGCGGCTCCAGCCCTCCCTTT 300
 DB 258 TCCGACCCCTCCCGGGTCCCGCCCGGAGCAGCCCTCCGCGGCTCCAGCCCTCCCTTT 317
 QY 301 CCTTTCGGGGCCCGCGCTCTCTCGGGGCGGAGTTTCAGGAGCGCTGGGTCTGCT 360
 DB 318 CCTTTCGGGGCCCGCGCTCTCTCGGGGCGGAGTTTCAGGAGCGCTGGGTCTGCT 377
 QY 361 GCGCAGCTGGGAGCGCTTCGGCGCCCGCGCCACCCCGCGC 397
 DB 378 GCGCAGCTGGGAGCGCTTCGGCGCCCGCGCCACCCCGCGC 414
 RESULT 4
 AAH41091
 ID AAH41091 standard; DNA; 3962 BP.
 XX AC AAH41091;
 XX 29-AUG-2001 (first entry)
 XX Telomerase reverse transcriptase (TERT) DNA.
 XX Phenotype switch molecule; phenotype-related gene battery;
 KW gene localisation; telomere reverse transcriptase; TERT; ds.
 XX Unidentified.
 OS WO200138515-A1.
 XX 31-MAY-2001.
 XX 17-NOV-2000; 2000WO-CN000427.
 XX 19-NOV-1999; 99CN-00121466.
 XX (BIAN/) BIAN X.
 XX Bian X;
 XX WPI; 2001-367684/38.
 XX Isolating phenotype switch molecules and phenotype-related gene batteries
 PT from complex genomes of higher animals and plants, useful e.g. in gene
 PT localization and classification analysis.
 XX Example 7; Page 27-29; 35pp; Chinese.

XX This invention relates to a method for isolating phenotype switch
 CC molecules and phenotype-related gene batteries from complex genomes of
 CC higher animals and plants. The method is useful in gene localisation and
 CC classification analysis, studying gene development networks and function
 CC networks, and designing drugs based on regulatory sequences of the
 CC phenotypes for disease treatment. The present sequence represents DNA
 CC encoding a telomere reverse transcriptase (TERT), which is used in an
 CC example illustrating the use of the method of the invention
 XX

SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;

Query Match 100.0%; Score 397; DB 4; Length 3962;
 Best Local Similarity 100.0%; Pred. No. 2e-56;
 Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCTGCTGGCGTCCCTGACCTCTGGAGCGCGGCGGGGGAAGCGCGC 60
 DB 3529 CCTCTGCTGGCGTCCCTGACCTCTGGAGCGCGGCGGGGGAAGCGCGC 3588

QY 61 CCAGACCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 120
 DB 3589 CCAGACCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 3648

QY 121 GATTGGGGGACAGAGCCCGGAGCGCGCTTCCACAGTGGGGAGGACTGGGAGCC 180
 DB 3649 GATTGGGGGACAGAGCCCGGAGCGCGCTTCCACAGTGGGGAGGACTGGGAGCC 3708

QY 181 GGGCACCCTGCTGCTCCCTTCACTTCCAGCTCCGCTCCGCGCGGACCCCGCCCG 240
 DB 3709 GGGCACCCTGCTGCTCCCTTCACTTCCAGCTCCGCTCCGCGCGGACCCCGCCCG 3768

QY 241 TCCGACCCCTTCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCCTCCAGCCCTTCCCTT 300
 DB 3769 TCCGACCCCTTCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCCTCCAGCCCTTCCCTT 3828

QY 301 CCTTTCCGGCGCCCGCTTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCT 360
 DB 3829 CCTTTCCGGCGCCCGCTTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCTGCT 3888

QY 361 GCGCAGCTGGGAAGCCCTGCGCCCGGCGCACCCCGCG 397
 DB 3889 GCGCAGCTGGGAAGCCCTGCGCCCGGCGCACCCCGCG 3925

RESULT 5
 AAA63785
 ID AAA63785 standard; DNA; 15418 BP.

AC AAA63785;

DT 04-DEC-2000 (first entry)

XX Nucleotide sequence of the human TERT promoter and gene from pGRN142.
 XX
 XX Telomerase reverse transcriptase; TERT; promoter; telomerase complex;
 XX telomere length; hyperplastic disease; cancer; oncolytic virus;
 XX cis-acting transcriptional control sequence; viral replication;
 XX cell proliferation; aging; immunological disorder; infertility; ss.
 XX Homo sapiens.

XX WO200046355-A2
 PD 10-AUG-2000.

XX 04-FEB-2000; 2000WO-US003104.

XX 04-FEB-1999; 99US-00244438.

XX (GERO-) GERON CORP.

PI Morin GB, Lichtsteiner S, Vasserot A, Adams R, Cardoza LM;

PI

XX Lebkowski JS;

XX WPI; 2000-532898/48.

XX New polynucleotides comprising cis-acting transcriptional control
 PT sequences, e.g. promoter sequence, of telomerase reverse transcriptase
 PT genes, useful in the treatment of cancer.

XX Claim 9; Page 58-61; 63pp; English.

XX The present sequence represents the human telomerase reverse
 CC transcriptase (TERT) promoter and gene. TERT is part of the telomerase
 CC complex responsible for maintaining telomere length and increasing
 CC replicative capacity of progenitor cells. Telomerase activity is turned
 CC off in mature differentiated cells, but is turned back on again in
 CC hyperplastic diseases, including many cancers. The polynucleotide
 CC comprises cis-acting transcriptional control sequences, e.g. promoter
 CC sequence. These promoter sequences are used to produce oncolytic viruses,
 CC in which a toxin or genetic element essential for viral replication is
 CC placed under the control of a TERT promoter. As a result, the virus
 CC replicates preferentially in cells expressing TERT, and selectively lyses
 CC cancer cells. The oncolytic viruses are useful for treating cancer in
 CC humans or animals. The TERT promoter sequences are useful in the
 CC treatment of cancer and other diseases of cell proliferation such as
 CC degenerative and aging processes and diseases of aging, immunological
 CC disorders, or infertility

SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 397; DB 3; Length 15418;

Best Local Similarity 100.0%; Pred. No. 1.6e-56;

Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTCGCTGGGTCTCCCTGACCTCTGGAGCGCGGCGCGGCGGGGGAAGCGCGC 60

DB 13148 CCCTCGCTGGGTCTCCCTGACCTCTGGAGCGCGGCGCGGCGGGGGAAGCGCGC 13207

QY 61 CCAGACCCCGGTCGCCCGGAGCAGCTGCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 120

DB 13208 CCAGACCCCGGTCGCCCGGAGCAGCTGCGCTGTGGGGCCAGGCCGGGCTCCCAAGTG 13267

QY 121 GATTGGGGGACAGAGCCCGGAGCGCGCTTCCACAGTGGGGAGGACTGGGAGCC 180

DB 13268 GATTGGGGGACAGAGCCCGGAGCGCGCTTCCACAGTGGGGAGGACTGGGAGCC 13327

QY 181 GGGCACCCTGCTGCTCCCTTCACTTCCAGCTCCGCTCCGCGCGGACCCCGCCCG 240

DB 13328 GGGCACCCTGCTGCTCCCTTCACTTCCAGCTCCGCTCCGCGCGGACCCCGCCCG 13387

QY 241 TCCGACCCCTTCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCCTCCAGCCCTTCCCTT 300

DB 13388 TCCGACCCCTTCCCGGTCGCCCGGAGCAGCTCGCTGTGGGGCCCTCCAGCCCTTCCCTT 13447

QY 301 CCTTTCCGGCGCCCGCTTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCT 360

DB 13448 CCTTTCCGGCGCCCGCTTCTCTCGCGGCGGAGTTTCAGGACGCTGCTGCTGCT 13507

QY 361 GCGCAGCTGGGAAGCCCTGCGCCCGGCGCACCCCGCG 397

DB 13508 GCGCAGCTGGGAAGCCCTGCGCCCGGCGCACCCCGCG 13544

RESULT 6

AAAL38601

ID AAAL38601 standard; DNA; 15418 BP.

XX AAAL38601;

XX 16-AUG-2002 (first entry)

XX Human TERT promoter and upstream sequence.

XX Cytostatic; glycosyltransferase; tumour; cell-surface carbohydrate;

KW tissue specific; transcriptional control element; cancer cell;
XX gene therapy; human TERT; telomerase reverse transcriptase; ds.
OS Homo sapiens.

PN WO200242468-A2.
XX
PD 30-MAY-2002.

XX
PF 26-NOV-2001; 2001WO-US044306.
XX

PR 27-NOV-2000; 2000US-0253395P.
XX

PA (GERO-) GERON CORP.
XX

PI Schiff MJ;
XX

DR WPI; 2002-479954/51.
XX

XX New polynucleotide encoding glycosyltransferase enzymes including histo
PT blood group transferase useful for treating conditions associated with
PT hyperproliferation, such as cancers and other neoplasias.

PS Claim 9; Page 17-20; 49pp; English.

XX The invention relates to a polynucleotide comprising an encoding sequence
CC for a glycosyltransferase, under control of a heterologous tumour
CC specific or tissue specific transcriptional control element, where
CC expression of the polynucleotide in a human cell causes the cell to
CC express a cell-surface carbohydrate determinant to which some or all
CC humans have a naturally occurring antibody. The polynucleotide of the
CC invention is useful for killing cancer cells and for preparing a
CC medicament for the treatment of cancer. The polynucleotide sequence of
CC the invention can be used to treat disorders by gene therapy. This
CC polynucleotide sequence represents the human TERT (telomerase reverse
CC transcriptase) promoter and upstream sequence related to the invention
XX

SQ Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;

Query Match 100.0%; Score 397; DB 6; Length 15418;
Beat Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCTCGTGGCGTCCCTGACACCTCGGAGCGGAGCGCGCGCGGCGGGAAGCGCGC 60
Db |||||
13148 CCCTCGTGGCGTCCCTGACACCTCGGAGCGGAGCGCGCGCGGCGGGAAGCGCGC 13207

QY 61 CCAGACCCCGGTCGCGCGCGGAGCGTGGCTGCGGGCCAGCGCGGCTCCCACTG 120
Db |||||
13208 CCAGACCCCGGTCGCGCGCGGAGCGTGGCTGCGGGCCAGCGCGGCTCCCACTG 13267

QY 121 GATTCCGGGACAGACGCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
Db |||||
13268 GATTCCGGGACAGACGCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327

QY 181 GGGCACCCGTCCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCG 240
Db |||||
13328 GGGCACCCGTCCTGCGCCCTTCACTTCCAGCTCCGCTCTCCGCGCGGACCCCGCCG 13387

QY 241 TCCGACCCCTTCCGGGTCGCGCGCGGACCGCCCTCCGGGCTCCGACCCCTCCCTT 300
Db |||||
13388 TCCGACCCCTTCCGGGTCGCGCGCGGACCGCCCTCCGGGCTCCGACCCCTCCCTT 13447

QY 301 CTTTTCGGGGCCCGCCCTCTCTCTCGCGCGCGAGTTTCAGGACGCGTGGTCTGCT 360
Db |||||
13448 CTTTTCGGGGCCCGCCCTCTCTCTCGCGCGCGAGTTTCAGGACGCGTGGTCTGCT 13507

QY 361 GGCACGTTGGGAAGCCCTGCGCCCGCGGACACCCCGCG 397
Db |||||
13508 GGCACGTTGGGAAGCCCTGCGCCCGCGGACACCCCGCG 13544

RESULT 7

ABS54997

ID ABS54997.standard; DNA; 15418 BP.

XX AC ABS54997;

XX DT 10-DEC-2002 (first entry)

XX DE Lambda clone containing human TERT genomic insert.

XX Telomerase reverse transcriptase; TERT; replication-conditional virus;
KW adenovirus replication gene; cancer cell; lung; pancreatic cancer;
KW medulloblastoma; cervical carcinoma; fibrosarcoma; osteosarcoma;
KW cytolysis; replication defective adenovirus vector; congenital defect;
KW proinflammatory; antiinflammatory; heterologous effector gene;
KW cancer therapy; cytostatic; gene therapy; lambda clone; human; ds.

XX Bacteriophage lambda.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FH FT misc_feature 1..43

FT /tag= a

FT /note= "From Lambda clone"

FT misc_feature 44..15375

FT /tag= b

FT /note= "Human telomerase reverse transcriptase (hTERT)
sequence including the hTERT promoter and upstream
sequence"

FT misc_feature 15376..15418

FT /tag= c

FT /note= "From Lambda clone"

FT WO200253760-A2.

XX 11-JUL-2002.

XX 17-DEC-2001; 2001WO-US048785.

XX 18-DEC-2000; 2000US-0256418P.

XX (GERO-) GERON CORP.

PI Irving JM, Lebkowski JS;

XX WPI; 2002-723123/78.

XX Novel replication-conditional virus useful for cytolysis of target cells
e.g. cancer cells and preparing a medicament for treating cancer,
PT comprises heterologous replication element in an adenovirus-based
PT construct.

XX Claim 11; Page 26-29; 32pp; English.

XX The present invention relates to a new replication-conditional virus with
CC a genome comprising adenovirus replication genes and one or more
CC heterologous gene(s) that functionally replaces one or more adenovirus
CC gene(s) required for replication or assembly of the virus. The invention
CC is useful for killing a cancer cell (such as lung, pancreatic cancer,
CC medulloblastoma, cervical carcinoma, fibrosarcoma or osteosarcoma),
CC killing a cell expressing TERT (telomerase reverse transcriptase), and in
CC preparing a medicament for treating cancer and a condition associated
CC with increased expression of TERT in affected cells, in a subject. The
CC invention is also useful for cytolysis of specific target cells. The
CC invention is further useful for producing replication defective
CC adenovirus vector which is useful for transient expression of a
CC heterologous therapeutic gene to correct a congenital defect, introducing
CC proinflammatory or antiinflammatory activity, enhancing telomerase
CC function, and delivering heterologous effector genes that induce killing
CC of the transduced cells. The invention is more safe for use in cancer
CC therapy. The present nucleic acid sequence represents the human TERT
CC sequence contained within a lambda clone sequence of the invention

XX

SQ	Sequence	15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
XX	Query Match	100.0%; Score 397; DB 6; Length 15418;
PT	Best Local Similarity	100.0%; Pred. No. 1.6e-56;
PT	Matches 397; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	Example 9; Page 62-66; 67pp; English.	
PS	The invention relates to a system for depleting a cell population of	
XX	undifferentiated stem cells, by introducing nucleic acids of structure P-	
CC	X, where X is a nucleic acid encoding product that is lethal to a cell in	
CC	which it is expressed; or renders a cell in which it is expressed	
CC	susceptible to the lethal effect of an external agent, and P is a	
CC	transcriptional control element causing X to be preferentially expressed	
CC	in the undifferentiated stem cells. The system is used for depleting a	
CC	cell population (preferably, human embryonic stem cells) of	
CC	undifferentiated stem cells. A population of differentiated cells is	
CC	useful in regenerative medicine, and for preparing antibodies and cDNA	
CC	libraries that are specific for a differentiated phenotype. The cell	
CC	populations are also useful for drug screening and therapeutic	
CC	applications. The differentiated cells are useful for tissue	
CC	reconstitution or regeneration in a human patient in need of treatment.	
CC	The cells are administered in a manner that permits to graft to the	
CC	intended tissue side and reconstitute or regenerate the functionally	
CC	deficient area. The neural progenitor cells are useful for treating acute	
CC	or chronic damage to the nerve system e.g. epilepsy, stroke, ischaemia,	
CC	Huntington's disease, Parkinson's disease, multiple sclerosis,	
CC	leukodystrophies, neuritis, etc. The hepatocytes and hepatocyte	
CC	precursors are useful for assessing animal models for ability to repair	
CC	liver damage. The cardiomyocyte population is useful for assessing animal	
CC	models for cryoinjury, regenerating cardiac muscle and to treat	
CC	insufficient cardiac function. This polynucleotide sequence represents	
CC	the DNA of plasmid pGRN144 containing the human hTERT gene relating to	
CC	the invention	
XX	Sequence	15418 BP; 4519 A; 3797 C; 3764 G; 3338 T; 0 U; 0 Other;
SQ	Query Match	100.0%; Score 397; DB 6; Length 15418;
XX	Best Local Similarity	100.0%; Pred. No. 1.6e-56;
XX	Matches 397; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGGCGCGGGGAGCGCGG 60
DB	13148	CCCTCGCTGGCGTCCCTGCACCCCTGGAGCGGAGCGGCGCGGGGAGCGCGG 13207
QY	61	CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCAGTG 120
DB	13208	CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGCTGTGGGGCCAGCGCGGCTCCAGTG 13267
QY	121	GATTGCGGGGACACAGCCCGCAGGACCGCGTTCCACGTGGCGGAGGACTGGGGACCC 180
DB	13268	GATTGCGGGGACACAGCCCGCAGGACCGCGTTCCACGTGGCGGAGGACTGGGGACCC 13327
QY	181	GGGACACCGTCTCTGGCCCTTACCTTCAGCTCCGCGCTCCCGCGGACCCCGCCCG 240
DB	13328	GGGACACCGTCTCTGGCCCTTACCTTCAGCTCCGCGCTCCCGCGGACCCCGCCCG 13387
QY	241	TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTTT 300
DB	13388	TCCCGACCCCTCCCGGGTCCCGCGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTTT 13447
QY	301	CCTTTCCCGGGCCCGCCCTCTCTTCGCGGGCGAGTTTCAGGACGCGTCTGCTCTGT 360
DB	13448	CCTTTCCCGGGCCCGCCCTCTCTTCGCGGGCGAGTTTCAGGACGCGTCTGCTCTGT 13507
QY	361	GCGCAGCTGGGAAGCCCTGGCCCGCGCCCGCCCGCCCG 397
DB	13508	GCGCAGCTGGGAAGCCCTGGCCCGCGCCCGCCCGCCCG 13544
RESULT 8	AAL38595	
ID	AAL38595 standard; DNA; 15418 BP.	
XX	AAL38595;	
XX	16-AUG-2002 (first entry)	
DE	DNA of plasmid pGRN144 containing human hTERT gene.	
KW	Anticonvulsant; cerebroprotective; vasotropic; nootropic; stem cell;	
KW	neuroprotective; antiparkinsonian; antiinflammatory; undifferentiated;	
KW	cardiant; transcriptional control element; human embryonic; tissue graft;	
KW	regenerative medicine; tissue reconstitution; neural progenitor cell;	
KW	nerve system; epilepsy; stroke; ischaemia; Huntington's disease;	
KW	Parkinson's disease; multiple sclerosis; leukodystrophy; neuritis;	
KW	hepatocyte; liver damage; cardiomyocyte; cryoinjury; cardiac muscle;	
KW	pGRN144; human hTERT gene; chimeric; db.	
OS	Homo sapiens.	
OS	Unidentified.	
OS	Chimeric.	
PN	WO200242445-A2.	
XX	30-MAY-2002.	
XX	26-NOV-2001; 2001WO-US044309.	
XX	27-NOV-2000; 2000US-0253357P.	
PR	27-NOV-2000; 2000US-0253443P.	
PR	13-FEB-2001; 2001US-00783203.	
XX	(GERO-) GERON CORP.	
XX	Gold JD, Lebrowski JS;	
PI	WPI; 2002-479952/51.	
DR	RESULT 9	
XX	ADC21253	
XX	ID ADC21253 standard; DNA; 15418 BP.	

XX AC ADC21253;
XX DT 18-DEC-2003 (first entry)
XX DE Lambda clone (lambdaGphi5) containing human TERT DNA.
XX KW Viral vector; heterologous control element; gene expression;
XX KW human telomerase reverse transcriptase; hTERT; tumour specific gene;
XX KW cell death; transcriptional control element;
XX KW human telomerase RNA component; hTR; cancer cell; liver cancer;
XX KW prostate cancer; muscle cancer; neural cell cancer; lung cancer;
XX KW pancreatic cancer; medulloblastoma; cervical carcinoma; fibrosarcoma;
XX KW osteosarcoma; lambda clone; lambdaGphi5; human; ds.
XX KW Synthetic.
OS Homo sapiens.
OS Bacteriophage lambda.
XX US2003099616-A1.
XX 29-MAY-2003.
XX 25-JUL-2002; 2002US-00206447.
XX 25-JUL-2001; 2001US-0308029P.
XX (IRVI/) IRVING J M.
XX (KARP/) KARP D B.
XX (SCHI/) SCHIFF J M.
XX Irving JM, Karpf DB, Schiff JM;
XX WPI; 2003-730140/69.
XX New dual specificity vectors driven by the telomerase promoter, useful
XX for killing or slowing the growth of tumor cells, or for treating cancer,
XX e.g. liver cancer, prostate cancer, lung cancer, or pancreatic cancer.
XX Example 1; Page 13-20; 25pp; English.
XX The present invention relates to a viral vector comprising first and
XX second genes controlled by heterologous control elements, where the first
XX gene is preferentially expressed in cells expressing human telomerase
XX reverse transcriptase (hTERT), and another gene under the control of a
XX heterologous transcriptional control element for a tissue or tumour
XX specific gene other than TERT, and where transduction of the vector into
XX a mammalian cell expressing TERT causes the death of the cell or its
XX progeny. In particular, the second gene may be under the control of a
XX transcriptional control element for a tissue specific gene selected from
XX albumin, alpha-fetoprotein, prostate-specific antigen, mitochondrial
XX creatine kinase, myelin basic protein, glial fibrillary acidic protein,
XX and neuron-specific enolase. The second gene may be under the control of
XX a transcriptional control element for a human telomerase RNA component
XX (hTR). The vector of the invention is useful for killing a cancer cell,
XX or treating a subject for a condition associated with increased
XX expression of TERT in affected cells. The vector is also useful in the
XX preparation of a medicament for treatment of a condition associated with
XX increased expression of TERT, particularly cancer, and especially liver
XX cancer, prostate cancer, muscle cancer, neural cell cancer, lung cancer,
XX pancreatic cancer, medulloblastoma, cervical carcinoma, fibrosarcoma, and
XX osteosarcoma. The present sequence represents a lambda clone
XX (lambdaGphi5) containing human TERT DNA.
XX Sequence 15418 BP; 4518 A; 3797 C; 3765 G; 3338 T; 0 U; 0 Other;
Query Match 100.0%; Score 397; DB 10; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCTCGTGGCTCCCTGCACCCCTGGAGCGCGCGCGCGCGGAGCGCGGC 60
DB 13148 CCCTCGTGGCTCCCTGCACCCCTGGAGCGCGCGCGCGCGGAGCGCGGC 13207

QY 61 CCAGACCCCGGGTCCGCGCGGACAGCTGGCTGTGCGGGCCAGGCGGGGCTCCCAAGT 120
DB 13208 CCAGACCCCGGGTCCGCGCGGAGCAGCTGGCTGTGCGGGCCAGGCGGGGCTCCCAAGT 13267
QY 121 GATTTCGGGGCACAGAGCCCGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 180
DB 13268 GATTTCGGGGCACAGAGCCCGGACCGCGCTTCCACGTGGCGGAGGACTGGGGACCC 13327
QY 181 GGGCACCCGCTCTGCGCCCTTCCACGCTCCGCGCTCTCCGCGGGGACCCCGCCCG 240
DB 13328 GGGCACCCGCTCTGCGCCCTTCCACGCTCCGCGCTCTCCGCGGGGACCCCGCCCG 13387
QY 241 TCCCGACCCCTTCCGCGGTCCCGGCGCCAGCCCTTCCGCGGCCCTCCAGCCCTTCCCTT 300
DB 13388 TCCCGACCCCTTCCGCGGTCCCGGCGCCAGCCCTTCCGCGGCCCTCCAGCCCTTCCCTT 13447
QY 301 CCTTTCGGGGCGCGCCGCTCTCCGCGGGCGGAGTTTCAGGCGAGGCTGGCTCCTGCT 360
DB 13448 CCTTTCGGGGCGCGCCGCTCTCCGCGGGCGGAGTTTCAGGCGAGGCTGGCTCCTGCT 13507
QY 361 GCGCACGTGGGAGCCCTTGGCCCGGCGCACCCCGCG 397
DB 13508 GCGCACGTGGGAGCCCTTGGCCCGGCGCACCCCGCG 13544

RESULT 10

ADI33422

ID ADI33422 standard; DNA; 455 BP.

XX AC ADI33422;

XX DT 22-APR-2004 (first entry)

XX DE Human telomerase promoter (hTERT) DNA SeqID 4.

XX KW human telomerase promoter; human; E1; E1A; IRES; E1B; anticancer;

XX KW cell death; cancer; cytostatic; ds.

XX OS Homo sapiens.

XX PN WO2004005511-A1.

XX PD 15-JAN-2004.

XX PF 07-JUL-2003; 2003WO-JP008573.

XX PR 08-JUL-2002; 2002JP-00198941.

XX PA (KANS-) KANSI TECHNOLOGY LICENSING ORG CO LTD.

XX PA (FUJI/) FUJIWARA T.

XX PA (TANA/) TANAKA N.

XX PA (KYOS/) KYO S.

XX PI Fujiwara T, Tanaka N, Kyo S, Shirakiya Y, Kawashima T;

XX WPI; 2004-099391/10.

XX PT Polynucleotide comprising a human telomerase promoter and an E1 gene for

XX treating cancer.

XX PS Example 1; SEQ ID NO 4; 34pp; Japanese.

XX CC This invention relates to a novel polynucleotide comprising a human

XX CC telomerase promoter and at least one viral E1 gene. Specifically, the E1

XX CC genes are E1A, IRES and E1B and the human telomerase promoter is

XX CC preferably hTERT. The present invention describes a virus containing this

XX CC polynucleotide and an anticancer agent that replicates efficiently in

XX CC tumour cells and causing cell death. As such, it can be used for the

XX CC treatment of cancer, in particular cancer of the stomach, large

XX CC intestine, lung, liver, prostate, pancreas, digestive tract, bladder,

XX CC mammary gland, uterus, thyroid gland and ovary. Accordingly, this

XX CC composition exhibits cytostatic activity. This polynucleotide sequence is

CC the human telomerase promoter (hTERT) DNA of the invention.

XX Sequence 455 BP; 41 A; 212 C; 142 G; 60 T; 0 U; 0 Other;

SQ Query Match 99.6%; Score 395.4; DB 12; Length 455;

Best Local Similarity 99.7%; Pred. No. 5.2e-56;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCGTGGCTCCCTGACACCTGGAGCGGAGCGCGCGGGGGAAGCGCGC 60

DB 59 CCTCTCGTGGCTCCCTGACACCTGGAGCGGAGCGCGCGGGGGAAGCGCGC 118

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTTCGGGGCCAGCCCGGGCTCCAGTG 120

DB 119 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTTCGGGGCCAGCCCGGGCTCCAGTG 178

QY 121 GATTTCGGGGCAAGACCGCCAGGACCGCGCTTCCACAGTGGGGAGGAGCTGGGGACCC 180

DB 179 GATTTCGGGGCAAGACCGCCAGGACCGCGCTTCCACAGTGGGGAGGAGCTGGGGACCC 238

QY 181 GGGCACCCGTCCTGCGGCTTCACTTCCAGCTCCGCTCTCTCGCGCGGACCCCGCCCG 240

DB 239 GGGCACCCGTCCTGCGGCTTCACTTCCAGCTCCGCTCTCTCGCGCGGACCCCGCCCG 298

QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCCCGCCAGCCCTCCCGGCGCTTCCAGCGCTTCCCTTT 300

DB 299 TCCGACCCCTCCCGGGTCCCGCGGAGCCCGCCAGCCCTCCCGGCGCTTCCAGCGCTTCCCTTT 358

QY 301 CCTTTTCGGGGCGCGCGCTTCTCTCGCGGGGAGTTTCAGGACGGCTGGTCTCTGCT 360

DB 359 CCTTTTCGGGGCGCGCGCTTCTCTCGCGGGGAGTTTCAGGACGGCTGGTCTCTGCT 418

QY 361 GCGCACGTGGGAAGCCCTGGCCCGCGCCACCCCGCGC 397

DB 419 GCGCACGTGGGAAGCCCTGGCCCGCGCCACCCCGCGC 455

RESULT 12

AAX88272

ID AAX88272 standard; DNA; 5126 BP.

AC AAX88272;

XX 22-SEP-1999 (first entry)

DT Human catalytic telomerase subunit 5'-flanking regulatory DNA.

DE Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;

XX modulator; telomerase regulatory region; cancer therapy; ss.

KW Homo sapiens.

XX DE19757984-A1.

PN 01-JUL-1999.

XX 24-DEC-1997; 97DE-01057984.

XX 24-DEC-1997; 97DE-01057984.

XX (FARB) BAYER AG.

XX Hagen G, Wick M, Zubov D;

XX WPI; 1999-372320/32.

XX New 5' flanking regulatory sequence from the human catalytic telomerase

PT subunit gene useful for cancer therapy.

XX Claim 1; Fig 4; 14pp; German.

XX This invention describes a novel 5' flanking regulatory sequence from the

CC human catalytic telomerase subunit gene. Recombinant constructs

CC containing the product of the invention can be linked with DNA encoding

XX an anti-tumour protein or reporter protein. The constructs are useful for

CC identifying candidate substances that modulate the activity of the

CC telomerase regulatory region. The constructs can be used in cancer

CC therapy

XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;

SQ Query Match 99.6%; Score 395.4; DB 2; Length 5126;

Best Local Similarity 99.7%; Pred. No. 3.5e-56;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCTCGTGGCTCCCTGACACCTGGAGCGGAGCGCGCGGGGGAAGCGCGC 60

DB 4727 CCTCTCGTGGCTCCCTGACACCTGGAGCGGAGCGCGCGGGGGAAGCGCGC 4785

QY 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTTCGGGGCCAGCCCGGGCTCCAGTG 120

DB 4787 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTTCGGGGCCAGCCCGGGCTCCAGTG 4846

QY 121 GATTTCGGGGCAAGACCGCCAGGACCGCGCTTCCACAGTGGGGAGGAGCTGGGGACCC 180

DB 4847 GATTTCGGGGCAAGACCGCCAGGACCGCGCTTCCACAGTGGGGAGGAGCTGGGGACCC 4906

QY 181 GGGCACCCGTCCTGCGGCTTCACTTCCAGCTCCGCTCTCTCGCGCGGACCCCGCCCG 240

DB 4907 GGGCACCCGTCCTGCGGCTTCACTTCCAGCTCCGCTCTCTCGCGCGGACCCCGCCCG 4966

QY 241 TCCGACCCCTCCCGGGTCCCGCGGAGCCCGCCAGCCCTCCCGGCGCTTCCAGCGCTTCCCTTT 300

DB 4967 TCCGACCCCTCCCGGGTCCCGCGGAGCCCGCCAGCCCTCCCGGCGCTTCCAGCGCTTCCCTTT 5026

QY 301 CCTTTTCGGGGCGCGCGCTTCTCTCGCGGGGAGTTTCAGGACGGCTGGTCTCTGCT 360

DB 5027 CCTTTTCGGGGCGCGCGCTTCTCTCGCGGGGAGTTTCAGGACGGCTGGTCTCTGCT 5086

QY 361 GCGCACGTGGGAAGCCCTGGCCCGCGCCACCCCGCGC 397

DB 5087 GCGCACGTGGGAAGCCCTGGCCCGCGCCACCCCGCGC 5123

RESULT 12

AAS96607

ID AAS96607 standard; DNA; 51552 BP.

AC AAS96607;

XX 09-APR-2002 (first entry)

DT DNA encoding human telomerase reverse transcriptase (TERT) #1.

DE Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;

XX cell growth inhibitor; antisense oligonucleotide; antisense technology;

XX ds.

OS Homo sapiens.

XX Key

FT Location/Qualifiers

FT 1..11492

FT /tag= a

FT /number= 1

FT 11274..47813

FT /tag= b

FT /product= "TERT"

FT /note= "Telomerase reverse transcriptase"

FT 11493..11596

FT /tag= c

FT /number= 1

FT 11597..12950

FT /tag= d

FT /number= 2

FT 12951..21566

FT /tag= e

```
FT exon /number= 2
FT 21567. .21762
FT /*tag= f
FT /number= 3
FT 21763. .23851
FT /*tag= g
FT /number= 3
FT 23852. .24032
FT /*tag= h
FT /number= 4
FT 24033. .24719
FT /*tag= i
FT /number= 4
FT 24720. .24899
FT /*tag= j
FT /number= 5
FT 24900. .25393
FT /*tag= k
FT /number= 5
FT 25394. .25549
FT /*tag= l
FT /number= 6
FT 25550. .30195
FT /*tag= m
FT /number= 6
FT 30196. .30292
FT /*tag= n
FT /number= 7
FT 30293. .31272
FT /*tag= o
FT /number= 7
FT 31273. .31358
FT /*tag= p
FT /number= 8
FT 31359. .33843
FT /*tag= q
FT /number= 8
FT 33844. .33957
FT /*tag= r
FT /number= 9
FT 33958. .35941
FT /*tag= s
FT /number= 9
FT 35942. .36013
FT /*tag= t
FT /number= 10
FT 36014. .37884
FT /*tag= u
FT /number= 10
FT 37885. .38073
FT /*tag= v
FT /number= 11
FT 38074. .41874
FT /*tag= w
FT /number= 11
FT 41875. .42001
FT /*tag= x
FT /number= 12
FT 42002. .42881
FT /*tag= y
FT /number= 12
FT 42882. .42943
FT /*tag= z
FT /number= 13
FT 42944. .46129
FT /*tag= aa
FT /number= 13
FT 46130. .46254
FT /*tag= ab
FT /number= 14
FT 46255. .47035
FT /*tag= ac
FT /number= 14
```

```
FT exon 47036. .47173
FT /*tag= ad
FT /number= 15
FT 47174. .47709
FT /*tag= ae
FT /number= 15
FT 47710. .50544
FT /*tag= af
FT /number= 16
XX WO200188198-A1.
XX 22-NOV-2001.
XX 15-MAY-2001; 2001WO-US015774.
XX 16-MAY-2000; 2000US-00572423.
XX 07-DEC-2000; 2000US-00733294.
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX WPI; 2002-075321/10.
XX P-PSDB; AAU72735.
```

New compound targeted to nucleic acid molecule encoding telomerase transcriptase (TERT), which specifically hybridizes with and inhibits expression of TERT, useful for modulating apoptosis and inhibiting cell growth.

Example 19; Page 112-138; 154pp; English.

The invention describes a compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human TERT (telomerase reverse transcriptase), where the compound specifically hybridizes with and inhibits the expression of TERT. A series of oligonucleotides were designed to target different regions of a central gap region consisting of nucleotides in length and composed of a central gap region consisting of ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-MOE) nucleotides. The compounds were analysed for their effect on human TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction (PCR). The compound is useful for inhibiting the expression of TERT in cells or tissues, for treating a human having disease or condition associated with TERT, for modulating apoptosis, for inhibiting cell growth (preferably, cancer cell growth), in antisense therapy and for diagnostics and therapeutics. This sequence encodes human telomerase reverse transcriptase (TERT) #1, and is used to create antisense oligonucleotides which modify TERT expression, described in the method of the invention

SQ Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;

Query Match 99.6%; Score 395.4; DB 6; Length 51552;
Best Local Similarity 99.7%; Pred. No. 2.4e-56;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGCGCGCGCGGAGCGCGGC 60
Db 10877 CCCTCGCTGGCGTCCCTGCACCTGGGAGCGCGCGCGCGCGGAGCGCGGC 10936
Qy 61 CCAGACCCCGGGTCCGCGCGCGAGCAGCTGCGCTGTGCGGGCCAGCGCGGCTCCAGTG 120
Db 10937 CCAGACCCCGGGTCCGCGCGCGAGCAGCTGCGCTGTGCGGGCCAGCGCGGCTCCAGTG 10956
Qy 121 GATTGGGGGACAGAGCCCGCAGGACCGCGCTTCCACGTCGCGGAGGAGACTGGGGACCC 180
Db 10997 GATTGGGGGACAGAGCCCGCAGGACCGCGCTTCCACGTCGCGGAGGAGACTGGGGACCC 11056
Qy 181 GGGCACCCTCTCCCTCCCTTCCCTTCCAGTCCGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 240
Db 11057 GGGCACCCTCTCTCCCTCCCTTCCCTTCCAGTCCGCTCCCTCCCTCCCTCCCTCCCTCCCT 11116
```



```
QY 241 TCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT 300
Db 11117 TCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT 11176
QY 301 CTTTCCCGGGCCCGCCCTCTCTCTCGCGGCGAGTTTCAGGCGGCTGCTGCT 360
Db 11177 CTTTCCCGGGCCCGCCCTCTCTCTCGCGGCGAGTTTCAGGCGGCTGCTGCT 11236
QY 361 GCGCAGTGGGAGCCCTCGCCCGGCGACCCCGCG 397
Db 11237 GCGCAGTGGGAGCCCTCGCCCGGCGACCCCGCG 11273

RESULT 13
ACC47272 standard; DNA; 378 BP.
XX AC ACC47272;
DT 11-AUG-2003 (first entry)
XX DE CEA gene cis-acting sequence.
XX KW Gene expression; promoter; cytostatic; gene therapy; antisense therapy;
XX KW cancer; cis-acting; CEA gene; ds.
XX OS Unidentified.
XX PN WO2003013555-A1.
XX PD 20-FEB-2003.
XX PF 05-AUG-2002; 2002WO-US024741.
XX PR 08-AUG-2001; 2001US-0310905P.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Fang B;
XX WPI; 2003-256488/25.
XX DR Expressing gene products in a cell type-preferential manner with a binary
XX PT or bicistronic expression system, useful for treating cancers of the
XX PT brain, head and neck, esophagus, thyroid, stomach, colon, liver,
XX PT prostate, skin and rectum.
XX PS Disclosure; Page 139; 141pp; English.
XX CC The invention relates to expressing gene product in a cell type-
XX CC preferential manner. The method involves providing a first expression
XX CC cassette having a cell type-preferential promoter, providing a second
XX CC expression cassette having an inducible promoter, and transferring the
XX CC first and second expression cassettes into a cell in which the cell type
XX CC -specific preferential promoter is active. The methods and compositions
XX CC of the present invention are useful for treating cancers of the brain,
XX CC head and neck, esophagus, thyroid, stomach, colon, liver, kidney,
XX CC prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The
XX CC present sequence represents a cis-acting sequence that confers expression
XX CC of the CEA gene
XX SQ Sequence 378 BP; 35 A; 178 C; 121 G; 44 T; 0 U; 0 Other;

Query Match 94.8%; Score 376.4; DB 8; Length 378;
Best Local Similarity 99.7%; Pred. No. 6.7e-53;
Matches 377; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 19 CACCTGGAGCGGAGCGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGC 78
Db 1 CACCTGGAGCGGAGCGCGCGCGGGGAGCGCGGCCAGACCCCGGGTCCGC 60
QY 79 CCGGAGCAGCTGCTGCTCGGGGCGAGCGCGGGCTCCAGTGGATTCCGGCGCACAGACG 138
```

```
Db 61 CCGGAGCAGCTGCGCTGTTCGGGGCCAGCCCGGGTCCAGTGGATTCCGGGCGACAGACG 120
QY 139 CCCAGGACCGGCTTCCCACTGGCGGAGGACTGGGACCCCGGACACCCGTCCTTGGCCCC 198
Db 121 CCCAGGACCGGCTTCCCACTGGCGGAGGACTGGGACCCCGGACACCCGTCCTTGGCCCC 180
QY 199 TTACCTTTCAGCTCCGCTCTCTCGCGCGGAGACCCCGGCGGCTCCGACCCCTCCCGGGT 258
Db 181 TTACCTTTCAGCTCCGCTCTCTCGCGCGGAGACCCCGGCGGCTCCGACCCCTCCCGGGT 240
QY 259 CCGGGCCAGCCCTCCGGGCGCTCCAGCCCTCCCTTCCCTTCCGGGGCCCGCC 318
Db 241 CCGGGCCAGCCCTCCGGGCGCTCCAGCCCTCCCTTCCCTTCCGGGGCCCGCC 300
QY 319 CTCTCTCGCGGCGAGTTTCAGGCGAGCTGCTGCTGCTGCGCACGTGGGAAGCCCT 378
Db 301 CTCTCTCGCGGCGAGTTTCAGGCGAGCTGCTGCTGCTGCGCACGTGGGAAGCCCT 360
QY 379 GCGCCCGGCGACCCCGCG 396
Db 361 GCGCCCGGCGACCCCGCG 378

RESULT 14
AAD27972/c
ID AAD27972 standard; DNA; 35871 BP.
XX AC AAD27972;
DT 16-JUL-2002 (first entry)
XX DE Recombinant adenovirus vector KD3-TERT.
XX KW Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;
XX KW human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;
XX KW cancer; KD3-TERT; EIA region; mutant; ds.
XX OS Mastadenovirus.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX PN US2002028785-A1.
XX PR 07-MAR-2002.
XX PF 19-SEP-2001; 2001US-00956335.
XX PR 12-JUL-1999; 99US-00351778.
XX PR 20-SEP-2000; 2000US-0233872P.
XX PA (UYSL-) UNIV SAINT LOUIS.
XX PI Wold WSM, Toth K, Tollefson AE, Kuppuswamy M;
XX WPI; 2002-328910/36.
XX PT Novel recombinant adenovirus vector useful for destroying neoplastic
XX PT cells, comprises a human telomerase reverse transcriptase promoter and at
XX PT least one inactivation mutation in the E3 region.
XX PS Claim 5; Page 28-44; 64pp; English.
XX CC The invention relates to a recombinant adenovirus vector which
XX CC overexpresses an adenovirus death protein (ADP) and which is replication-
XX CC restricted to cells expressing telomerase, comprises a human telomerase
XX CC reverse transcriptase promoter (hTERT) and at least one inactivating
XX CC mutation in the E3 region. The vector of the invention is useful in vitro
XX CC for promoting death of a cell expressing telomerase, and for promoting
XX CC death of neoplastic cells in a patient. The adenovirus vector is an
XX CC efficient and effective anticancer agent that could specifically target
XX CC neoplastic cells, while replicating poorly or not at all in normal
```


CC tissue, and efficiently spreading to neighbouring neoplastic cells,
CC thereby maximising its cancer-killing ability. The presence of human
CC telomerase reverse transcriptase promoter allows restriction of
CC replication of the adenovirus to cells expressing telomerase without the
CC need for complementation to achieve replication competence in these
CC cells. The present sequence is adenovirus vector KD3-TERT which comprises
CC an ADP gene, a hTERT promoter, and a mutation in the E1A region
XX
SQ Sequence 35871 BP; 8238 A; 10114 C; 10001 G; 7518 T; 0 U; 0 Other;
Query Match 89.2%; Score 354.2; DB 6; Length 35871;
Best Local Similarity 99.2%; Pred. No. 1.3e-49;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGGTCTCTGACCTCGGAGCGGAGCGGCGGCGGGAAGCGCGC 60
Db 34385 CCCTCGCTGGGTCTCTGACCTCGGAGCGGAGCGGCGGGAAGCGCGC 34326
QY 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCGGCTCCAGTG 120
Db 34325 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCGGCTCCAGTG 34266
QY 121 GATTCCGGGGCACAGACCCCGAGGACCGCTTCCACGTGCGGAGGACTGGGGACCC 180
Db 34265 GATTCCGGGGCACAGACCCCGAGGACCGCTTCCACGTGCGGAGGACTGGGGACCC 34206
QY 181 GGGACCCCGTCTGCGCCCTTCCACCTTCCAGCTCGGCTCTCCGCGGACCCCGCCCG 240
Db 34205 GGGACCCCGTCTGCGCCCTTCCACCTTCCAGCTCGGCTCTCCGCGGACCCCGCCCG 34146
QY 241 TCCCGACCCCTCCGGGTCCCGGCGGACCCCTTCCGGGCGCTCCGAGCCCTCCCTTT 300
Db 34145 TCCCGACCCCTCCGGGTCCCGGCGGACCCCTTCCGGGCGCTCCGAGCCCTCCCTTT 34086
QY 301 CCTTTCCGGCGCCCGCCCTCTCCTCGGCGGCGAGTTTCAGGCAGCGCTGGCTCTGC 359
Db 34085 CCTTTCCGGCGCCCGCCCTCTCCTCGGCGGCGAGTTTCAGGCAGCGCTGATTACTGC 34027
RESULT 15
AAD27971/c
ID AAD27971 standard; DNA; 35978 BP.
XX
AC AAD27971;
XX
DT 16-JUL-2002 (first entry)
XX
DE Recombinant adenovirus vector GZ3-TERT.
XX
KW Recombinant adenovirus vector; adenovirus death protein; ADP; telomerase;
KW human; telomerase reverse transcriptase promoter; TERT; neoplastic cell;
KW cancer; GZ3-TERT; E3 region; mutant; ds.
XX
OS Mastadenovirus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
FN US2002028785-A1.
XX
PD 07-MAR-2002.
XX
PF 19-SEP-2001; 2001US-00956335.
XX
PR 12-JUL-1999; 99US-00351778.
PR 20-SEP-2000; 2000US-0233872P.
XX
PA (UYSL-) UNIV SAINT LOUIS.
XX
PI Wold WSM, Toth K, Tollefsen AE, Kuppaswamy M;
XX
DR WPI; 2002-328910/36.
XX

PT Novel recombinant adenovirus vector useful for destroying neoplastic
PT cells, comprises a human telomerase reverse transcriptase promoter and at
PT least one inactivation mutation in the E3 region.
XX
PS Claim 2; Page 12-28; 64pp; English.
XX
CC The invention relates to a recombinant adenovirus vector which
CC overexpresses an adenovirus death protein (ADP) and which is replication-
CC restricted to cells expressing telomerase, comprises a human telomerase
CC reverse transcriptase promoter (hTERT) and at least one inactivating
CC mutation in the E3 region. The vector of the invention is useful in vitro
CC for promoting death of a cell expressing telomerase, and for promoting
CC death of neoplastic cells in a patient. The adenovirus vector is an
CC efficient and effective anticancer agent that could specifically target
CC neoplastic cells, while replicating poorly or not at all in normal
CC tissue, and efficiently spreading to neighbouring neoplastic cells,
CC thereby maximising its cancer-killing ability. The presence of human
CC telomerase reverse transcriptase promoter allows restriction of
CC replication of the adenovirus to cells expressing telomerase without the
CC need for complementation to achieve replication competence in these
CC cells. The present sequence is adenovirus vector GZ3-TERT which comprises
CC an ADP gene, a hTERT promoter, and a mutation in the E3 region
XX
SQ Sequence 35978 BP; 8265 A; 10141 C; 10026 G; 7546 T; 0 U; 0 Other;
Query Match 89.2%; Score 354.2; DB 6; Length 35978;
Best Local Similarity 99.2%; Pred. No. 1.3e-49;
Matches 356; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCCTCGCTGGGTCTCTGACCTCGGAGCGGAGCGGCGGCGGGAAGCGCGC 60
Db 34492 CCCTCGCTGGGTCTCTGACCTCGGAGCGGAGCGGCGGGAAGCGCGC 34433
QY 61 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCGGCTCCAGTG 120
Db 34432 CCAGACCCCGGGTCCGCGGAGCAGCTGCGCTGTGGGGCCAGGCGGCTCCAGTG 34373
QY 121 GATTCCGGGGCACAGACCCCGAGCAGCGCTTCCACGTGCGGAGGACTGGGGACCC 180
Db 34372 GATTCCGGGGCACAGACCCCGAGCAGCGCTTCCACGTGCGGAGGACTGGGGACCC 34313
QY 181 GGGACCCCGTCTGCGCCCTTCCACCTTCCAGCTCGGCTCTCCGCGGACCCCGCCCG 240
Db 34312 GGGACCCCGTCTGCGCCCTTCCACCTTCCAGCTCGGCTCTCCGCGGACCCCGCCCG 34253
QY 241 TCCCGACCCCTCCGGGTCCCGGCGGACCCCTTCCGGGCGCTCCAGCCCTTCCCTT 300
Db 34252 TCCCGACCCCTCCGGGTCCCGGCGGACCCCTTCCGGGCGCTCCAGCCCTTCCCTT 34193
QY 301 CCTTTCCGGCGCCCGCCCTCTCCTCGGCGGCGAGTTTCAGGCAGCGCTGGCTCTGC 359
Db 34192 CCTTTCCGGCGCCCGCCCTCTCCTCGGCGGCGAGTTTCAGGCAGCGCTGATTACTGC 34134

Search completed: April 9, 2005, 06:08:12
Job time : 422.17 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:56:54 ; Search time 1998.54 Seconds
(without alignments)
4666.271 Million cell updates/sec

Title: US-10-081-969-94

Perfect score: 245

Sequence: 1 cccacgtggcggaggact.....tggccccggccacccccgcg 245

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_ges1:*
- 9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	77.2	31.5	1285	9 AG334095	AG334095 Mus muscu
C 2	75.8	30.9	1695	8 CC290874	CC290874 CH261-172
C 3	75.4	30.8	941	9 CL465224	CL465224 SAIL_1236
C 4	75	30.6	566	9 CNS03JNO	AL247077 Tetradon
C 5	74.4	30.4	881	5 BX427015	BX427015 BX427015
C 6	74.4	30.4	969	9 CL477043	CL477043 SAIL_267
C 7	74.4	30.4	988	9 CL477397	CL477397 SAIL_272
C 8	73.8	30.1	468	5 BQ608819	BQ608819 BRY_4732
C 9	73.6	30.0	794	8 BZ050856	BZ050856 jnr64f12
C 10	73.6	30.0	1233	9 AG341138	AG341138 Mus muscu
C 11	73.4	30.0	949	9 CL465953	CL465953 SAIL_1249
C 12	73.4	30.0	1270	9 AG382572	AG382572 Mus muscu
C 13	73.2	29.9	1081	9 CL464716	CL464716 SAIL_1225
C 14	72.8	29.7	759	9 AG126157	AG126157 Pan trogl
C 15	72.6	29.6	675	8 BZ050815	BZ050815 jnr64a12
C 16	72.6	29.6	897	9 CL459907	CL459907 SAIL_104
C 17	72.4	29.6	1400	9 AG429585	AG429585 Mus muscu
C 18	72.4	29.6	1531	9 AG430426	AG430426 Mus muscu
C 19	72.2	29.5	1197	4 BI416470	BI416470 hasp001xa
C 20	72.2	29.5	1449	9 AG360973	AG360973 Mus muscu
C 21	72	29.4	1008	9 AG395157	AG395157 Mus muscu
C 22	71.8	29.3	1289	9 CL447104	CL447104 ISB1-156E
C 23	71.6	29.2	458	9 CNS0002T	AL060559 Drosophil
C 24	71.6	29.2	944	9 AG062271	AG062271 Pan trogl

ALIGNMENTS

RESULT 1
AG334095/c
LOCUS Mus musculus molossinus DNA, clone:MSMg01-124N12.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG334095
VERSION AG334095.1 GI:47907405
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1285)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@sc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@tc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@tc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY : pBACe3.6
Vector : EcoRI
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES
source
1..1285 Location/Qualifiers
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-124N12.TJ"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

```

ORIGIN
Query Match          31.5%; Score 77.2; DB 9; Length 1285;
Best Local Similarity 58.0%; Pred. No. 7e-05;
Matches 127; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 26 CCGGGGACCGGTCCTTCCAGCTTCCAGCTCGGCTCTCTCCGCGGACCCCGCC 85
DB 845 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 786

QY 86 CCCTCCCGACCCCTCCCGGTCCTCCCGGCGAGCCCTCTCCGCGCCCTCCAGCCCTCC 145
DB 785 CGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 726

QY 146 CTTCTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 205
DB 725 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 666

QY 206 GCTGCGCAGCTGGGAAGCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 244
DB 665 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 627

RESULT 2
LOCUS CC290874 1695 bp DNA linear GSS 13-MAY-2003
DEFINITION CH261-172N5_Sp6.1 CH261 Gallus gallus genomic clone CH261-172N5,
ACCESSION CC290874
VERSION CC290874.1 GI:30662315
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1695)
AUTHORS Warren, W., Graves, T., Mardis, E. and Wilson, R.,
Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Kremitzki, C.,
TITLE Gallus gallus BAC End Reads
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submission@wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTAGTGACACTATAG
Class: BAC ends
High quality sequence start: 26
High quality sequence stop: 136.
FEATURES
Location/Qualifiers
1..1695
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-172N5"
/sex="female"
/cell_line="UCD001, inbred 256"
/notes="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - for library and clone
ordering information: http://www.chori.org/bacpac"

ORIGIN
Query Match          30.9%; Score 75.8; DB 8; Length 1695;
Best Local Similarity 57.3%; Pred. No. 0.0012;
Matches 125; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 26 CCGGGGACCGGTCCTTCCAGCTTCCAGCTCGGCTCTCTCCGCGGACCCCGCC 85
DB 1420 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1479

ORIGIN
Query Match          30.8%; Score 75.4; DB 9; Length 941;
Best Local Similarity 56.9%; Pred. No. 0.00016;
Matches 136; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 7 GTGGGCGAGGACTGGGGACCCGCGGACCCGTCCTTCACCTTCAGCTCCGCT 66
DB 608 GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667

QY 67 CTTCCGCGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
DB 668 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727

QY 127 GGCCTTCCAGGCGCTTCCCTTCTTTCGCGCGCGCGCGCGCGCGCGCG 186
DB 728 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787

```


LOCUS CL477043 969 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_267_A03.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_267_A03.v1, genomic survey sequence.
ACCESSION CL477043
VERSION CL477043.1 GI:45943329
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 969)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS812359; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.

FEATURES
source
1..969
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone_lib="SAIL_267_A03.v1"
/clone_lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match 30.4%; Score 74.4; DB 9; Length 969;
Best Local Similarity 57.5%; Pred. No. 0.00024;
Matches 126; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
QY 26 CCGGGGACCCGTCCTGCCCCCTTACCTTCCAGCTCCGCTCTCCGGGGGAGACCCCGCC 85
DB 531 CCCCCCCCCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC 590
QY 86 CCGTCCGACCCCTCCGGGTCCCGGCCAGCCCTCCGGGCTCCAGCCCTCCG 145
DB 591 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 650
QY 146 CTTCTTTCCGGCGCCCGCCCTCTCTCTCCGGCGCGAGTTTCAGGCAGCGCTGCGTCT 205
DB 651 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 710
QY 206 GCTGCGACGTGGGAAGCCCTTGGCCCGCGGCACCCCCCGC 244
DB 711 CGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 749

RESULT 7
CL477397
LOCUS CL477397 988 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_272_B09.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_272_B09.v1, genomic survey sequence.
ACCESSION CL477397
VERSION CL477397.1 GI:45944169
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)

LOCUS CL477043 969 bp DNA linear GSS 01-APR-2004
DEFINITION SAIL_267_A03.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_267_A03.v1, genomic survey sequence.
ACCESSION CL477043
VERSION CL477043.1 GI:45943329
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 988)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
TITLE A high-throughput Arabidopsis reverse genetics system
JOURNAL Plant Cell 14 (12), 2985-2994 (2002)
MEDLINE 22356987
PUBMED 12468722
COMMENT Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS812603; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.

FEATURES
source
1..988
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone_lib="SAIL_272_B09.v1"
/clone_lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match 30.4%; Score 74.4; DB 9; Length 988;
Best Local Similarity 56.3%; Pred. No. 0.00024;
Matches 138; Conservative 0; Mismatches 107; Indels 0; Gaps 0;
QY 1 CCCCACGTGGGGAGGGAGTGGGGACCCGGGACCCGTCCTGCTCCCTTCCAGCTTCCAGCT 60
DB 429 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 488
QY 61 CCGCTCTCTCCGCGGGACCCCGCCCGGTCCTCCGACCCCTCCCGGGTCCCGGCCAGCCC 120
DB 489 CCGCGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 548
QY 121 CTTCCGGGCTTCCAGGCCCCCTCCCTTCTTTCGGGGCCCCGCTCTCTCTCGGGCG 180
DB 549 CCCCCCGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 608
QY 181 CGAGTTTTCAGGCAGCGCTCGCTCTGCTCGCACGTGGGAAGCCCTTGGGCCCGCCACC 240
DB 609 GCGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 668
QY 241 CCGCG 245
DB 669 CCGCG 673

RESULT 8
BQ608819/c
LOCUS BQ608819 468 bp mRNA linear EST 25-JUN-2002
DEFINITION BRY_4732 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.
ACCESSION BQ608819
VERSION BQ608819.1 GI:21558158
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;


```
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .1233
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-134L24.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

FEATURES
source
1. .949
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_1249_G02.v1"
/clone_lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match 30.0%; Score 73.4; DB 9; Length 949;
Best Local Similarity 57.1%; Pred. No. 0.00037;
Matches 125; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 26 CCGGGGACCGCTCTCGGCTTCCAGCTCCGCTCCGCGGCGGACCCCGCC 85
DB 478 CNTNNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 537
QY 86 CGGTCCCGACCCCTCCCGGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 145
DB 538 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 597
QY 146 CTTCTTTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 205
DB 598 CCNCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 597
QY 206 GCTGGCGACGTGGGAAGCCCTGGGCGGCGGCGGCGGCGGCGGCGGCGG 244
DB 658 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 657

RESULT 12
AG382572 1270 bp DNA linear GSS 03-JUN-2004
AG382572 Mus musculus molossinus DNA, clone:MSMg01-133C09.T7, genomic survey
sequence.
AG382572.1 GI:47993777
GSS.
Mus musculus molossinus
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1270)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
Library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .1270
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

FEATURES
source
1. .1233
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-134L24.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match 30.0%; Score 73.6; DB 9; Length 1233;
Best Local Similarity 58.5%; Pred. No. 0.00033;
Matches 127; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 26 CCGGGGACCGCTCTCGGCTTCCAGCTCCGCTCCGCGGCGGACCCCGCC 85
DB 569 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC 628
QY 86 CGGTCCCGACCCCTCCCGGCTCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 145
DB 629 CCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 688
QY 146 CTTCTTTTCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 205
DB 689 CCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 748
QY 206 GCTGGCGACGTGGGAAGCCCTGGGCGGCGGCGGCGGCGGCGGCGGCGG 242
DB 749 GCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 785

RESULT 11
CL465953 949 bp DNA linear GSS 31-MAR-2004
LOCUS
DEFINITION
SAIL_1249_G02.v1 SAIL Collection Arabidopsis thaliana genomic clone
SAIL_1249_G02.v1, genomic survey sequence.
CL465953
VERSION
KEYWORDS
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 949)
Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miquel,T., Hutchison,D., Kimmerly,B.,
Mitzel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
22356987
12468722
Contact: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS846032; T-DNA left border flanking sequences of
Syngenta Arabidopsis insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: T-DNA tagged
Location/Qualifiers

FEATURES
source
1. .1270
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
```



```
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-193C09.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match          30.0%; Score 73.4; DB 9; Length 1270;
Best Local Similarity 56.1%; Pred. No. 0.00036;
Matches 137; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 1 CCCACGTGGCGAGGACTGGGACCCGGGACCCGCTCTGCTCCCTTCACCTTCAGCT 60
Db 864 CCCCCCGCGGCCCCCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 923
QY 61 CGCCTCTCTCCGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 924 CCCCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 983
QY 121 CCTCGGGGCTTCAGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Db 984 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1043
QY 181 CGAGTTTACGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
Db 1044 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1103
QY 241 CGCG 244
Db 1104 CCCC 1107

RESULT 13
LOCUS CL464716 1081 bp DNA linear GSS 31-MAR-2004
DEFINITION SAIL_1225_G10.v1 SAIL Collection Arabidopsis thaliana genomic clone
ACCESSION CL464716
VERSION CL464716.1 GI:45867621
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1081)
AUTHORS Sessions,A., Burke,E., Presting,G., Aux,G., McElver,J., Patton,D.,
Dietrich,B., Ho,P., Bacwaden,J., Ko,C., Clarke,J.D., Cotton,D.,
Bullis,D., Snell,J., Miguel,T., Hutchison,D., Kimmerly,B.,
Mittel,T., Katagiri,F., Glazebrook,J., Law,M. and Goff,S.A.
COMMENT A high-throughput Arabidopsis reverse genetics system
Plant Cell 14 (12), 2985-2994 (2002)
22356987
12468722
PUBMED
CONTACT: Sessions A
Applied Trait Genetics
Syngenta Biotechnology Inc.
3054 Cornwallis Rd., Research Triangle Park, NC 27709, USA
Email: allen.sessions@syngenta.com
ABRC Stock Number CS94896; T-DNA left border flanking sequences of
Syngenta Arabidopsis Insertion Library (SAIL) lines are available
through the Arabidopsis Biological Resource Center (ABRC).
Sequences represent a pool of amplified genomic regions and not
single contiguous sequences.
Class: TDNA tagged.
FEATURES
source
1..1081
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="SAIL_1225_G10.v1"

/clone_lib="SAIL Collection"
/note="T-DNA left border sequences were isolated using a
modified TAIL-PCR strategy"

ORIGIN
Query Match          29.9%; Score 73.2; DB 9; Length 1081;
Best Local Similarity 56.5%; Pred. No. 0.0004;
Matches 135; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 7 GTGGCGGAGGACTGGGACCCGGGACCCGCTCTCTCTCTCTCTCTCTCTCTCT 66
Db 387 GGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446
QY 67 CTTGCGCGGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
Db 447 CCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506
QY 127 GGCCCTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186
Db 507 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566
QY 187 TCAGCGACGCTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245
Db 567 CCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 625

RESULT 14
LOCUS AG126157 759 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-136K03.F, genomic survey sequence.
ACCESSION AG126157
VERSION AG126157.1 GI:16655322
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
COMMENT BAC end sequences of Library PTB
2 (bases 1 to 759)
Unpublished
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbeg@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI.
R.Site 2 : SacI.
Location/Qualifiers
1..759
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-136K03.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

Query Match          29.7%; Score 72.8; DB 9; Length 759;
Best Local Similarity 55.7%; Pred. No. 0.00049;
```


1	397	100.0	397	6	AX817857	Sequence
2	397	100.0	2043	9	AF098956	Homo sapi
3	397	100.0	4321	6	AF098956	Sequence
4	397	100.0	4356	9	AF097365	Homo sapi
5	397	100.0	15332	9	AF121948	Homo sapi
6	397	100.0	15418	6	AR342806	Sequence
7	397	100.0	15418	6	AR490112	Sequence
8	397	100.0	15418	6	AX453025	Sequence
9	397	100.0	15418	6	AX498409	Sequence
10	397	100.0	15418	6	AX504952	Sequence
11	397	100.0	92564	9	AY007685	Homo sapi
12	397	100.0	161252	2	AC114955	Homo sapi
13	397	100.0	202305	6	AC114391	Homo sapi
14	395.4	99.6	5126	6	AX003120	Sequence
15	395.4	99.6	5491	9	AB016767	Homo sapi
16	395.4	99.6	11276	6	AX003122	Sequence
17	395.4	99.6	26414	9	HS2ERT1	Homo sapi
18	395.4	99.6	51552	6	AC3666023	Sequence
19	382.8	96.4	170646	2	AC123545	Pan trogl

Db	181	GGGACCCCGTCTGCGCCCTTACCTTCAGCTCCGCTCTCCGCGCGGACCCCGCCCG	240
Qy	241	TCGGACCCCTCCCGGTTCCCGGCCAGCCCTCCCGGCCCTCCAGCCCTCCGCTT	300
Db	241	TCGGACCCCTCCCGGTTCCCGGCCAGCCCTCCCGGCCCTCCAGCCCTCCGCTT	300
Qy	301	CTTTTCGGGGCCCGCCCTCTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCT	360
Db	301	CTTTTCGGGGCCCGCCCTCTCTCTCGCGCGGAGTTTCAGGCAGCGCTGCTGCT	360
Qy	361	GGCAGCTGGGAGCCCTCGCCCGCGCCACCCCGCG	397
Db	361	GGCAGCTGGGAGCCCTCGCCCGCGCCACCCCGCG	397
RESULT 2			
AF098956			
LOCUS			
DEFINITION			
Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter			
region and partial cds.			
ACCESSION			
AF098956			
VERSION			
AF098956.1			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
REFERENCE			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 2043)			
Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.			
Cloning and characterization of the promoter region of human			
telomerase reverse transcriptase gene			
Cancer Res. 59 (4), 826-830 (1999)			
JOURNAL			
MEDLINE			
PUBMED			
10029071			
2 (bases 1 to 2043)			
Horikawa,I., Cable,P.L., Afshari,C. and Barrett,J.C.			
Direct Submission			
TITLE			
Submitted (15-OCT-1998) Laboratory of Molecular Carcinogenesis,			
National Institute of Environmental Health Sciences, 111 T. W.			
JOURNAL			
Alexander Drive, P.O. Box 12233, Research Triangle Park, NC 27709,			
USA			
FEATURES			
source			
1..2043			
/organism="Homo sapiens"			
/mol_type="genomic DNA"			
/db_xref="taxon:9606"			
/chromosome="5"			
/map="5p15.33"			
1..>2043			
/genes="TERT"			
gene			
1..1665			
/genes="TERT"			
promoter			
1666..>1939			
/genes="TERT"			
mRNA			
/product="telomerase reverse transcriptase"			
1721..>1939			
/genes="TERT"			
CDS			
/note="catalytic subunit"			
/codon_start=1			
/product="telomerase reverse transcriptase"			
/protein_id="AA012786.1"			
/db_xref="GI:4226059"			
/translations="MPRAPRCRAVRSLLRSHYREVLPLATFVRLGFGQWRLLVQRGDP			
AAFRALVAQLVCVPWDARPPPAAPSRQ"			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
397; Conservative			
0; Mismatches			
0; Indels			
0; Gaps			
0;			
Qy	1	CCCTCGCTGGCGTCCCTGCACCTTGGGAGCGGAGCGCGCGCGGGGGAAGCGCGC	60
Db	1324	CCCTCGCTGGCGTCCCTGCACCTTGGGAGCGGAGCGCGCGCGGGGGAAGCGCGC	1383

Qy	361	CGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG	397	
Db	2446	CGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCGCG	2482	
RESULT 4				
AF097365		4356 bp	DNA	linear
LOCUS	AF097365			PRI 02-FEB-1999
DEFINITION	Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter and partial cds.			
ACCESSION	AF097365			
VERSION	AF097365.1	GI:4210970		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 4356)			
AUTHORS	Cong, Y.S., Wen, J. and Bacchetti, S.			
TITLE	The human telomerase catalytic subunit hTERT: organization of the gene and characterization of the promoter			
JOURNAL	Hum. Mol. Genet. 8 (1), 137-142 (1999)			
MEDLINE	99105927			
PUBMED	9887342			
REFERENCE	2 (bases 1 to 4356)			
AUTHORS	Cong, Y.S., Wen, J. and Bacchetti, S.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main St. W., Hamilton, ON L8N 3Z5, Canada			
FEATURES	Location/Qualifiers			
source	1. .4356			
gene	/organism="Homo sapiens"			
promoter	/mol_type="genomic DNA"			
mRNA	/db_xref="taxon:9606"			
CDS	/chromosome="5"			
ORIGIN	1. .>4356			
Query Match	100.0%; Score 397; DB 9; Length 4356;			
Best Local Similarity	100.0%; Pred. No. 3.6e-49;			
Matches 397; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCCTCGCTGGGTCCCTGACCCCTGGAGCGGCGCGCGCGGCGGAGCGCGCG	60	
Db	3600	CCCTCGCTGGGTCCCTGACCCCTGGAGCGGCGGCGCGGCGGAGCGCGCG	3659	
Qy	61	CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGCTGTGCGGGCGCAGCGCGGCTCCAGTG	120	
Db	3660	CCAGACCCCGGGTCCGCGCGGAGCAGCTGCGCTGTGCGGGCGCAGCGCGGCTCCAGTG	3719	
Qy	121	GATTGCGGGGACAGACGCCCGAGGACCGCGCTTCCACGTGCGGAGGACCTGGGGACCC	180	
Db	3720	GATTGCGGGGACAGACGCCCGAGGACCGCGCTTCCACGTGCGGAGGACCTGGGGACCC	3779	
Qy	181	GGGACCCGCTCTGCGCCCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT	240	
Db	3780	GGGACCCGCTCTGCGCCCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCTTCCAGCT	3839	
RESULT 5				
AF121948		15332 bp	DNA	linear
LOCUS	AF121948			PRI 11-APR-1999
DEFINITION	Homo sapiens telomerase reverse transcriptase (TERT) gene, partial cds.			
ACCESSION	AF121948			
VERSION	AF121948.1	GI:4580662		
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 15332)			
AUTHORS	Greenberg, R.A., O'Hagan, R.C., Deng, H., Xiao, Q., Hann, S.R., Adams, R.R., Lichtsteiner, S., Chin, L., Morin, G.B. and DePinho, R.A.			
TITLE	Telomerase reverse transcriptase gene is a direct target of c-Myc but is not functionally equivalent in cellular transformation			
JOURNAL	Oncogene 18 (5), 1219-1226 (1999)			
MEDLINE	99144726			
PUBMED	10022128			
REFERENCE	2 (bases 1 to 15332)			
AUTHORS	Morin, G.B., Carlos, R. and Adams, R.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive, Menlo Park, CA 94025, USA			
FEATURES	Location/Qualifiers			
source	1. .15332			
gene	/organism="Homo sapiens"			
promoter	/mol_type="genomic DNA"			
mRNA	/db_xref="taxon:9606"			
CDS	1. .>15332			
ORIGIN	1. .13446			
Query Match	100.0%; Score 397; DB 9; Length 15332;			
Best Local Similarity	100.0%; Pred. No. 2.3e-49;			
Matches 397; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	CCCTCGCTGGGTCCCTGACCCCTGGAGCGGCGGCGGCGGAGCGCGCG	60	

Db 13105 CCTTGGCTGGCTCCTGACACCTGGAGCGCGAGCGCGCGGGAGCGCGC 13164
Qy 61 CCAGACCCCGGGTCCGCGGAGAGCTGCGCTGTGCGGGCCAGCGCGGGTCCAGTG 120
Db 13165 CCAGACCCCGGGTCCGCGGAGAGCTGCGCTGTGCGGGCCAGCGCGGGTCCAGTG 13224
Qy 121 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 180
Db 13225 GATTGCGGGCACAGACGCCAGGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 13284
Qy 181 GGGACACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 240
Db 13285 GGGACACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 13344
Qy 241 TCCGACCCCTTCCGGGTCCGCGGCCAGCGCCCTCCGCGGCCCTCCAGCCCTCCCTT 300
Db 13345 TCCGACCCCTTCCGGGTCCGCGGCCAGCGCCCTCCGCGGCCCTCCAGCCCTCCCTT 13404
Qy 301 CTTTCCGGGCGCCCGCTTCTCTCGCGGCGAGTTTCAGGACGCTGCTGCT 360
Db 13405 CTTTCCGGGCGCCCGCTTCTCTCGCGGCGAGTTTCAGGACGCTGCTGCT 13464
Qy 361 GCGCAGCTGGGAAGCCCTGGCCCGCGCCACCCCGCG 397
Db 13465 GCGCAGCTGGGAAGCCCTGGCCCGCGCCACCCCGCG 13501

RESULT 6
LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells
JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
FEATURES
Location/Qualifiers
source 1..15418
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 397; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGTGGCTCCCTGCACTCCCTGGAGCGCGAGCGCGCGGGGAGCGCGC 60
Db 13148 CCCTCGTGGCTCCCTGCACTCCCTGGAGCGCGAGCGCGCGGGGAGCGCGC 13207
Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCAGTG 120
Db 13208 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCAGTG 13267
Qy 121 GATTGCGGGCACAGACGCCAGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGCACAGACGCCAGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 13327
Qy 181 GGGACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 240
Db 13328 GGGACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 13387
Qy 241 TCCGACCCCTTCCGGGTCCCGGCCAGCGCCCTTCCGCGGCTTCCAGCCCTTCCCTT 300
Db 13388 TCCGACCCCTTCCGGGTCCCGGCCAGCGCCCTTCCGCGGCTTCCAGCCCTTCCCTT 13447
Qy 301 CTTTCCGGGCGCCCGCTTCTCTCGGGCGCGAGTTTCAGGACGCTGCTGCT 360

Db 13448 CCTTTCGGCGCGCGCGCTTCTCTCGCGCGCGAGTTTCAGGACGCTGCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGGCCCGCGCGACCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGGCCCGCGCGACCCCGCG 13544
RESULT 7
LOCUS AR490112 15418 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713055.
ACCESSION AR490112
VERSION AR490112.1 GI:47257268
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Schiff,J.M.
TITLE Glycosyltransferase vectors for treating cancer
JOURNAL Patent: US 6713055-A 1 30-MAR-2004;
FEATURES
Location/Qualifiers
source 1..15418
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 397; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCTCGTGGCTCCCTGCACTCCCTGGAGCGCGAGCGCGCGGGGAGCGCGC 60
Db 13148 CCCTCGTGGCTCCCTGCACTCCCTGGAGCGCGAGCGCGCGGGGAGCGCGC 13207
Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCAGTG 120
Db 13208 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGTGTGCGGGCCAGCGCGGCTCCAGTG 13267
Qy 121 GATTGCGGGCACAGACGCCAGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 180
Db 13268 GATTGCGGGCACAGACGCCAGACCGCGCTTCCACAGTGGCGAGGACTGGGGACCC 13327
Qy 181 GGGACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 240
Db 13328 GGGACCCCTGCTGCCCTTCACTTCCAGCTCCGCTTCTCCGCGGACCCCGCCCG 13387
Qy 241 TCCGACCCCTTCCGGGTCCCGGCCAGCGCCCTTCCGCGGCTTCCAGCCCTTCCCTT 300
Db 13388 TCCGACCCCTTCCGGGTCCCGGCCAGCGCCCTTCCGCGGCTTCCAGCCCTTCCCTT 13447
Qy 301 CTTTTCGGCGCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGACGCTGCTGCT 360
Db 13448 CTTTTCGGCGCGCGCGCTTCTCTCGGGCGCGAGTTTCAGGACGCTGCTGCT 13507
Qy 361 GCGCAGCTGGGAAGCCCTGGCCCGCGCGACCCCGCG 397
Db 13508 GCGCAGCTGGGAAGCCCTGGCCCGCGCGACCCCGCG 13544

RESULT 8
LOCUS AX453025 15418 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0242445.
ACCESSION AX453025
VERSION AX453025.1 GI:21712594
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

* 1 3008: contig of 3008 bp in length
* 3009 3108: gap of unknown length
* 3109 9208: contig of 6101 bp in length
* 9210 9309: gap of unknown length
* 9310 15613: contig of 6304 bp in length
* 15614 15713: gap of unknown length
* 15713 23243: contig of 7530 bp in length
* 23244 23343: gap of unknown length
* 23344 39674: contig of 16331 bp in length
* 39675 39774: gap of unknown length
* 39775 60001: contig of 20227 bp in length
* 60002 60101: gap of unknown length
* 60102 85303: contig of 25202 bp in length
* 85304 85403: gap of unknown length
* 85404 117450: contig of 32057 bp in length
* 117461 117561: gap of unknown length
* 117561 161252: contig of 43692 bp in length.
FEATURES
source
1. .161252
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-117B23"
/clone_lib="RPC1 human BAC library 11"
ORIGIN
Query Match 100.0%; Score 397; DB 2; Length 161252;
Best Local Similarity 100.0%; Pred. No. 1e-49; 0; Indels 0; Gaps 0;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTCGTGGCGTCCCTGACACCTGGAGCGGAGCGGCGGCGGCGGAGCGCGC 60
Db 136937 CCTCGTGGCGTCCCTGACACCTGGAGCGGAGCGGCGGCGGAGCGCGC 136878
Qy 61 CCAGACCCCGGGTCCCGCGGAGCGTGGCTGTCGGGGCCAGCGCGGGCTCCAGTG 120
Db 136877 CCAGACCCCGGGTCCCGCGGAGCGTGGCTGTCGGGGCCAGCGCGGGTCCAGTG 136818
Qy 121 GATTGGGGGACAGACCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGACCC 180
Db 136817 GATTGGGGGACAGACCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGACCC 136758
Qy 181 GGGCACCCGCTCTGCCCTTACCTTCCAGCTCGGCTCTCCGCGGAGACCCGCGCG 240
Db 136757 GGGCACCCGCTCTGCCCTTACCTTCCAGCTCGGCTCTCCGCGGAGACCCGCGCG 136698
Qy 241 TCCGACCCCTTCCCGGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 136697 TCCGACCCCTTCCCGGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 136638
Qy 301 CTTTTCGCGGCGCGCGCTCTCTCTCGGCGGCGAGTTTTCAGGACGCGTTCGCTTCTGT 360
Db 136637 CTTTTCGCGGCGCGCGCTCTCTCTCGGCGGCGAGTTTTCAGGACGCGTTCGCTTCTGT 136578
Qy 361 GCGCAGCTGGGAAGCCTTGGCCCGGCGACCCCGCG 397
Db 136577 GCGCAGCTGGGAAGCCTTGGCCCGGCGACCCCGCG 136541
RESULT 13
AC114291/c 202305 bp DNA linear PRI 15-MAR-2003
LOCUS Homo sapiens chromosome 5 clone CTD-3080P12, complete sequence.
DEFINITION AC114291
ACCESSION AC114291
VERSION AC114291.2 GI:28973811
KEYWORDS Htg.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 202305)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
Unpublished
2 (bases 1 to 202305)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 202305)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (15-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 15, 2003 this sequence version replaced gi:19224940.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.sbgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: Transposon sequencing failed to verify number of repeat
copies 173000-175780. Unsure number of repeat copies 173000-175780.
BAC and subclones unstable 76080. Force join at 76080.
FEATURES
source
1. .202305
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-3080P12"
76080
/note="NOTE: BAC and subclones unstable 76080. Force join
at 76080."
misc_feature
173000..175780
/note="NOTE: Transposon sequencing failed to verify number
of repeat copies 173000-175780. Unsure number of repeat
copies 173000-175780"
ORIGIN
Query Match 100.0%; Score 397; DB 9; Length 202305;
Best Local Similarity 100.0%; Pred. No. 9.5e-50;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTCGTGGCGTCCCTGACACCTGGAGCGGAGCGGCGGCGGAGCGCGC 60
Db 179393 CCTCGTGGCGTCCCTGACACCTGGAGCGGAGCGGCGGAGCGCGC 179334
Qy 61 CCAGACCCCGGGTCCCGCGGAGCGTGGCTGTCGGGGCCAGCGGGCTCCAGTG 120
Db 179333 CCAGACCCCGGGTCCCGCGGAGCGTGGCTGTCGGGGCCAGCGGGTCCAGTG 179274
Qy 121 GATTGGGGGACAGACCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGACCC 180
Db 179273 GATTGGGGGACAGACCGCCAGGACCGCGCTTCCACGTGGCGGAGGACTGGGACCC 179214
Qy 181 GGGCACCCGCTCTGCCCTTACCTTCCAGCTCCGCTCTCTCCGCGGAGACCCCGCGCG 240
Db 179213 GGGCACCCGCTCTGCCCTTACCTTCCAGCTCCGCTCTCTCCGCGGAGACCCCGCGCG 179154
Qy 241 TCCGACCCCTTCCCGGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 179153 TCCGACCCCTTCCCGGGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGG 179094
Qy 301 CTTTTCGCGGCGCGCGCTCTCTCTCGGCGGCGAGTTTTCAGGACGCGTTCGCTTCTGT 360
Db 179093 CTTTTCGCGGCGCGCGCTCTCTCTCGGCGGCGAGTTTTCAGGACGCGTTCGCTTCTGT 179034
Qy 361 GCGCAGCTGGGAAGCCTTGGCCCGGCGACCCCGCG 397
Db 179033 GCGCAGCTGGGAAGCCTTGGCCCGGCGACCCCGCG 178997
RESULT 14
AX003120

LOCUS AX003120 5126 bp DNA linear PAT 24-AUG-2000
ACCESSION Sequence 1 from Patent WO9933998.
VERSION AX003120.1 GI:9926982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wick, M. and Hagen, G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
JOURNAL Patent: WO 9933998-A 1 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
source Location/Qualifiers
1. 5126
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.6%; Score 395.4; DB 6; Length 5126;
Best Local Similarity 99.7%; Pred. No. 5.8e-49;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCTCGCTGGCGTCCCTGCACCTCTGGAGCGAGCGCGCGCGGGGGAAGCGCGC 60
Db 4727 CCTCGCTGGCGTCCCTGCACCTCTGGAGCGAGCGCGCGCGGGGGAAGCGCGC 4786
Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGTGGCTGTCTGGGGCCAGCGCGGCTCCAGTG 120
Db 4787 CCAGACCCCGGGTCCCGCGGAGCAGTGGCTGTCTGGGGCCAGCGCGGCTCCAGTG 4846
Qy 121 GATTTCGGGGCAGACAGCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 180
Db 4847 GATTTCGGGGCAGACAGCCCGAGACCGCGCTTCCACGTGGCGAGGAGCTGGGGACCC 4906
Qy 181 GGGCACCGCTCTCGCCCTTCACTTCCAGTCCGCTCTCTCCGCGGAGCCCGCCCGC 240
Db 4907 GGGCACCGCTCTCGCCCTTCACTTCCAGTCCGCTCTCTCCGCGGAGCCCGCCCGC 4966
Qy 241 TCCGACCCCTCCGGTCCCGGGCCAGCCCTTCCGGGCGCTCCAGCCCTCCCGCTT 300
Db 4967 TCCGACCCCTCCGGTCCCGGGCCAGCCCTTCCGGGCGCTCCAGCCCTCCCGCTT 5026
Qy 301 CTTTTCGGCGCCCGCGCTCTCTTCGGGGCGAGTTTTCAGGAGCGCTCGTCTCTGCT 360
Db 5027 CTTTTCGGCGCCCGCGCTCTCTTCGGGGCGAGTTTTCAGGAGCGCTCGTCTCTGCT 5086
Qy 361 GCGCAGTGGGAAGCCCTGGCCCGCCAGCCCGCCAGCCCGCGC 397
Db 5087 GCGCAGTGGGAAGCCCTGGCCCGCCAGCCCGCCAGCCCGCGC 5123
RESULT 15
LOCUS AB016767 5491 bp DNA linear PRI 29-JAN-2002
DEFINITION Homo sapiens gene for telomerase transcriptase, partial cds.
ACCESSION AB016767
VERSION AB016767.1 GI:4239869
KEYWORDS telomerase transcriptase; hTERT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Takakura, M., Kyo, S., Kanaya, T., Hirano, H., Takeda, J., Yutsudo, M.
TITLE Cloning of human telomerase catalytic subunit (hTERT) gene promoter
and identification of proximal core promoter sequences essential
for transcriptional activation in immortalized and cancer cells
JOURNAL Cancer Res. 59 (3), 551-557 (1999)

MEDLINE 99137484
PUBMED 9973199
REFERENCE 2 (bases 1 to 5491)
AUTHORS Takakura, M., Kyo, S., Kanaya, T., Takeda, J. and Inoue, M.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University,
School of Medicine, Department of Obstetrics and Gynecology; 13-1,
Takaramachi, Kanazawa, Ishikawa 920-0934, Japan
(E-mail: takakura@med.kanazawa-u.ac.jp, Tel: 81-76-265-2425,
Fax: 81-76-234-4266)
FEATURES
source Location/Qualifiers
1. 5491
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
3250..3255
/note="telomerase transcriptase promoter"
3331..3336
/note="telomerase transcriptase promoter"
3338..5491
/gene="hTERT"
3338..3633
/gene="hTERT"
/number=1
3338..3414
/gene="hTERT"
/evidence="experimental"
join(3415..3633, 3738..5088)
/gene="hTERT"
/codon_start=1
/product="telomerase transcriptase"
/protein_id="BAA74724.1"
/db_xref="GI:4239870"
/translation="MPAPRCRAVRSLLRSHYREVLPLATFVRRLGQWRLVQRGDP
AALFALVAQCLVCPWPDPAPPAAPSPVQVSLKELVARLQRLCERAKXVLAFGFA
LPPARGGPEAFTTSVRSYLPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFV
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRLGCRANVHSVREAGVPLGLPA
PGARRGGSASRLPLPRRGAAPERTPVQGSWAHPGRTGRGSDRGFCVVSFA
RPAEATSLGALSGLRSHPSVGRQHAGPPSTSRPPMDTFCPPVYAKTKHFLYS
SGKEQLRPSFLSLSLPILTGARLVETIFLAGSPCGQLPAGCPACPSATGKGCPC
FWCGLGTRSAPTGCSRRTARCELRSPPQVSPVGRSPRALMRPPRRRTOTPVAMCS
CSASTAPLAGVLRAGLPAPAGAPRPLGLQAQRRLFLNTKFI SLGHAKLSLQELT
WMSVRDCAWLRSP"
3634..3737
/gene="hTERT"
/number=1
3738..5088
/gene="hTERT"
/number=2
5089..5491
/gene="hTERT"
/number=2
ORIGIN
Query Match 99.6%; Score 395.4; DB 9; Length 5491;
Best Local Similarity 99.7%; Pred. No. 5.6e-49;
Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCTCGCTGGCTCCCTGCACCTTGGGAGCGCGAGCGCGCGGGGGAAGCGCGC 60
Db 3018 CCCTCGCTGGCTCCCTGCACCTTGGGAGCGCGAGCGCGGGGGAAGCGCGC 3077
Qy 61 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTCTGGGGCCAGCGCGGCTCCAGTG 120
Db 3078 CCAGACCCCGGGTCCCGCGGAGCAGCTGCGCTGTCTGGGGCCAGCGCGGCTCCAGTG 3137
Qy 121 GATTTCGGGGCAGACAGCCCGAGACCGCGCTTCCACGTGGCGGAGGAGCTGGGGACCC 180
Db 3138 GATTTCGGGGCAGACAGCCCGAGACCGCGCTTCCACGTGGCGGAGGAGCTGGGGACCC 3197
Qy 181 GGGCACCGCTCTCGCCCTTCACTTCCAGTCCGCTCTCTCCGCGGAGCCCGCCCGC 240
Db 3198 GGGCACCGCTCTCGCCCTTCACTTCCAGTCCGCTCTCTCCGCGGAGCCCGCCCGC 3257

Qy	241	TCCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT	300
Db	3258	TCCCGACCCCTCCCGGGTCCCGGGCCAGCCCTCCCGGGCCCTCCAGCCCTCCCTT	3317
Qy	301	CCTTTCCGGGGCCCGCCCTCTCTCGGGCGCGAGTTTCAGGCAGCGCTGCGTCTGCT	360
Db	3318	CCTTTCCGGGGCCCGCCCTCTCTCGGGCGCGAGTTTCAGGCAGCGCTGCGTCTGCT	3377
Qy	361	GCGCAGTGGGAAGCCCTGGCCCGGCCACCCCGCG	397
Db	3378	GCGCAGTGGGAAGCCCTGGCCCGGCCACCCCGCG	3414

Search completed: April 9, 2005, 07:02:06
 Job time : 1999.42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 04:29:03 ; Search time 256.83 Seconds
(without alignments)
5647.064 Million cell updates/sec

Title: US-10-081-969-94

Perfect score: 245

Sequence: 1 cccacgtggcggaggact.....tggccccgccacccccgcg 245

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1990s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	245	ABS98659	Human TER
2	245	100.0	261	ABK12706	Human tel
3	245	100.0	295	ABV75307	Telomeras
4	245	100.0	295	ABV75306	TERT mini
5	245	100.0	295	ABZ23897	TERT mini
6	245	100.0	455	ADI33422	Human tel
7	245	100.0	955	ABS98580	ARI7PAE2f
8	245	100.0	5126	AAH88272	Human cat
9	245	100.0	5928	ABK12707	Minimal t
10	245	100.0	51552	AAH96607	DNA encod
11	244	99.6	378	ACC47272	CEA gene
12	244	99.6	397	ABS98658	Human TER
13	244	99.6	408	ADR73423	Human tel
14	244	99.6	902	ADR73427	Human m-h
15	244	99.6	3962	AAH41091	Telomeras
16	244	99.6	15418	3 AA63785	Nucleotid
17	244	99.6	15418	6 AAL38601	Human TER
18	244	99.6	15418	6 ABS54997	Lambda cl
19	244	99.6	15418	6 AAL38595	DNA of pl
20	244	99.6	15418	10 ADC21253	Lambda cl

21	237.4	96.9	327	6	AAL55438	Aal55438 Specific
22	237.4	96.9	327	12	ADI80429	Adi80429 Anti-tumo
23	236	96.3	293	6	AAL55435	Aal55435 Specific
24	236	96.3	293	6	ABQ76069	Abq76069 Anticance
25	229.8	93.8	314	3	AA94134	Aa94134 Telomeras
26	205	83.7	240	10	ABZ23898	Abz23898 Telomeras
27	205	83.7	454	11	ADN00285	Adn00285 Tumour-sp
28	201.2	82.1	35871	6	AAD27972	Aad27972 Recombina
29	201.2	82.1	35978	6	AAD27971	Aad27971 Recombina
30	200.8	82.0	403	6	ABS98583	Abs98583 Ari7PAE2f
31	199.8	81.6	4335	2	AAV16979	Aav16979 Human tel
32	198	80.8	1677	6	AAD27973	Aad27973 Human tel
33	183.2	74.8	4356	6	ABL92335	AbL92335 Chemical
34	158.6	64.7	1404	6	AAD22344	Aad22344 Chemical
35	144	58.8	144	8	ABZ79850	Abz79850 TERT mini
36	89	36.3	4356	6	ABL92334	AbL92334 Chemical
37	88	35.9	89	6	ABV73905	Abv73905 Telomeras
38	77	31.4	78	6	ABV74896	Abv74896 Minimal t
39	77	31.4	78	8	ABZ79851	Abz79851 Human sit
40	77	31.4	78	10	ABZ22591	Abz22591 Human TER
41	69.4	28.3	1404	6	AAD22343	Aad22343 Chemical
42	67	27.3	600	6	ABQ52497	Abq52497 Oligonucl
43	67	27.3	600	6	ABQ52496	Abq52496 Oligonucl
44	66.8	27.3	1416	8	ABZ20967	Abz20967 Animal te
45	66.6	27.2	28198	10	ADG37080	Adg37080 Mouse pla

ALIGNMENTS

RESULT 1

ID	ABS98659	standard; DNA; 245 BP.
XX	ABS98659;	
AC	ABS98659;	
XX	17-DEC-2002	(first entry)
DT	Human TERT promoter sequence #2.	
DE	Human TERT promoter sequence #2.	
XX	Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;	
KW	inverted terminal repeat; ITR; termination signal sequence; lung cancer;	
KW	E2F responsive promoter; adenoviral packaging signal; prostate cancer;	
KW	neoplastic condition; colon cancer; cytostatic; immunostimulant;	
KW	gene therapy; human; TERT; promoter; ds.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200267861-A2.	
PN	06-SEP-2002.	
PD	06-SEP-2002.	
XX	22-FEB-2002; 2002WO-US005300.	
PF	23-FEB-2001; 2001US-0270922P.	
XX	01-JUN-2001; 2001US-0295037P.	
PR	14-JAN-2002; 2002US-0348670P.	
XX	(NOVS) NOVARTIS PHARMA AG.	
PA	Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CW;	
XX	Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;	
PI	Police SR, Clarke L, Phipps S, Cheng C;	
XX	WPI; 2002-705950/76.	
DR	Recombinant viral vector comprising an adenoviral nucleic acid backbone,	
XX	useful for treating neoplastic disorders such as lung, breast, prostate	
PT	or colon cancer.	
XX	Claim 11; Page 21; 226pp; English.	
PS	The present invention relates to a new recombinant viral vector	
XX		
CC		

CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX
SQ Sequence 245 BP; 18 A; 127 C; 66 G; 34 T; 0 U; 0 Other;
Query Match 100.0%; Score 245; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 4.5e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 60
Db 1 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 60
QY 61 CGCCTCTCCGCGGACCCCGCGTCCCGACCCCTCCGGGTCCCGGCCAGCCC 120
Db 61 CGCCTCTCCGCGGAGACCCCGCGTCCCGACCCCTCCGGGTCCCGGCCAGCCC 120
QY 121 CTTCCGGGCTCCAGACCCCTCCCTTCTTTCGCGGCGCCCGCTCTCTCGCGCG 180
Db 121 CTTCCGGGCTCCAGACCCCTCCCTTCTTTCGCGGCGCCCGCTCTCTCGCGCG 180
QY 181 CGAGTTTCAGGACGCTCGTCTGCTGGGACGTCGGAAGCCCTGGCGCCACCC 240
Db 181 CGAGTTTCAGGACGCTCGTCTGCTGGGACGTCGGAAGCCCTGGCGCCACCC 240
QY 241 CCGCG 245
Db 241 CCGCG 245
RESULT 2
ID ABK12706 standard; DNA; 261 BP.
XX
AC ABK12706;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human telomerase reverse transcriptase (TERT) minimal promoter sequence.
XX
KW Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn;
KW repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer;
KW acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis;
KW skin rejuvenation; immune senescence; bone marrow transplant; skin graft;
KW neoplastic disease; TERT minimal promoter; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 171..211
FT /tag= a
FT /label= Target site_C domain
FT /note= "Specifically claimed in claim 37"
FT 5'UTR 182..259
FT /tag= c
FT /note= "A portion of the 5' untranslated region"
FT misc_feature 182..209
FT /tag= b
FT /note= "Repressor site"
FT misc_feature 190..210
FT /tag= e
FT /note= "Specifically claimed in claim 37"
FT misc_feature 190..202
FT /tag= d
FT /note= "Specifically claimed in claim 37"

FT misc_feature 191..201
FT /tag= f
FT /note= "E2F transcription factor binding site consensus
FT sequence, E2F-Q6"
FT misc_feature 192..201
FT /tag= g
FT /note= "Specifically claimed in claim 37"
PN WO200216657-A1.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-US025861.
XX
PR 24-AUG-2000; 2000US-0227865P.
PR 01-SEP-2000; 2000US-0230174P.
PR 05-OCT-2000; 2000US-0239345P.
XX
XX (SIER-) SIERRA SCI INC.
PI Andrews WH, Foster CA, Fraser S, Mohammadpour H;
XX WPI; 2002-280952/32.
DR
XX
PT Modulating expression of telomerase reverse transcriptase (TERT) in a
PT cell, for regulating proliferative capacity of a cell, involves
PT modulating TERT transcription repression by Site C repressor binding
PT site.
XX
PS Disclosure; Fig 1; 66pp; English.
XX
CC The present invention relates to a new method of modulating expression of
CC telomerase reverse transcriptase (TERT) from a TERT expression system
CC that includes a TERT promoter and a Site C repressor binding site. The
CC method of the invention involves modulating TERT transcription repression
CC by the Site C repressor binding site. The method of the invention is
CC useful for modulating expression of TERT for producing a mammalian
CC antibody. The method is also useful in a variety of different
CC applications, including immortalisation of cells, production of reagents
CC for use in life science research, therapeutic applications, and
CC therapeutic agent screening applications. Increasing TERT expression
CC delays natural telomeric shortening and/or increases telomeric length and
CC is useful for treating disease conditions such as Progeria or Hutchinson-
CC Gilford syndrome, acquired immunodeficiency syndrome (AIDS),
CC cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit
CC immune senescence. The method can be employed to lengthen telomeres of
CC osteoblast and osteoclast stem cells, encouraging bone replacement and
CC proper remodeling and reinforcement, and can thus be used in bone marrow
CC transplants for the treatment of cancer and skin grafts for burn victims
CC and as such the method improves the survival and effectiveness of bone
CC marrow and skin cell transplants. Decreasing TERT expression is useful
CC for treating cellular proliferative disease conditions, including
CC neoplastic disease conditions e.g. cancer. The present nucleic acid
CC sequence represents the human TERT minimal promoter sequence of the
CC invention
XX
SQ Sequence 261 BP; 21 A; 133 C; 71 G; 36 T; 0 U; 0 Other;
Query Match 100.0%; Score 245; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.4e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 60
Db 14 CCCACGTGGCGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 73
QY 61 CGCCTCTCCGCGGACCCCGCGTCCCGACCCCTCCGGGTCCCGGCCAGCCC 120
Db 74 CGCCTCTCTCCGCGGAGACCCCGCCGCTCCCGACCCCTCCGGGTCCCGGCCAGCCC 133
QY 121 CTTCCGGGCTCCAGACCCCTCCCTTCTTTCGCGGCGCCCGCTCTCTCGCGCG 180
Db 134 CTTCCGGGCTCCAGACCCCTCCCTTCTTTCGCGGCGCCCGCTCTCTCGCGCG 193

QY 181 CGAGTTTCAGGACGGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGCCCGGCGCACCC 240
 |||||
 Db 194 CGAGTTTCAGGACGGCTGCGTCTGCTGCGCACTGGGAAGCCCTGCGCCCGGCGCACCC 253

QY 241 CCGCG 245
 |||||
 Db 254 CCGCG 258

RESULT 3
 ABV75307
 ID ABV75307 standard; DNA; 295 BP.
 AC
 XX
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE Telomerase minimal promoter sequence.
 XX
 XX TERT; telomerase reverse transcriptase; TF-8; TF-13; telomerase;
 KW cardiovascular; osteopathic; virucide; transcription; promoter; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200290570-A2.
 PN
 XX
 XX 14-NOV-2002.
 PD
 XX
 XX 07-MAY-2002; 2002WO-US014720.
 PF
 XX
 XX 08-MAY-2001; 2001US-0289717P.
 PR
 XX
 XX (SIERRA) SIERRA SCI INC.
 PA
 XX
 XX Andrews WH;
 PI
 XX WPI; 2003-103520/09.
 DR
 XX
 XX New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor
 PT binding site, useful in regulating TERT expression and for screening
 PT agents that modulate TERT transcription repressing activity of the TF-8
 PT and TF-13 sites.
 XX
 PS Example; Page 31; 40pp; English.
 XX
 CC The invention relates to a new telomerase reverse transcriptase (TERT) TF
 -8 and/or TF-13 repressor binding site. The nucleic acid comprising the
 CC binding site sequence is useful in preparing constructs, such as vectors
 CC and expression systems, and probes for the TERT TF-8 and/or TF-13
 CC repressor binding site in non-human animals. Modulating the transcription
 CC repressing activity of TERT TF-8 and/or TF-13 repressor factors to
 CC regulate telomerase expression, can be used in immortalization of cells,
 CC production of reagents useful in life science research, and therapeutic
 CC research. Inhibitors of TERT transcription repression by a TF-8 and/or TF
 -13 repressor may be used for increasing the proliferative capacity of a
 CC cell, and for treating Progeria, Hutchinson-Gilford syndrome,
 CC cardiovascular disease, osteoporosis, or AIDS. The present sequence
 CC represents the telomerase minimal promoter
 XX
 SQ Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
 Query Match 100.0%; Score 245; DB 8; Length 295;
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGCT 60
 |||||
 Db 36 CCCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGCT 95

QY 61 CCGCTCTCTCCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 120
 |||||
 Db 96 CCGCTCTCTCCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 155

QY 121 CCTCCGGGCGCTCCAGCCCTCCCTTCTTTCCGGGCGCCCGCCCTCTCTCTGCGGCG 180
 |||||
 Db 156 CCTCCGGGCGCTCCAGCCCTCCCTTCTTTCCGGGCGCCCGCCCTCTCTCTGCGGCG 215

QY 181 CGAGTTTCAGGACGGCTGCGTCTGCGCACTGGGAAGCCCTGCGCCCGGCGCACCC 240
 |||||
 Db 216 CGAGTTTCAGGACGGCTGCGTCTGCGCACTGGGAAGCCCTGCGCCCGGCGCACCC 275

QY 241 CCGCG 245
 |||||
 Db 276 CCGCG 280

RESULT 4
 ABV75306
 ID ABV75306 standard; DNA; 295 BP.
 AC
 XX
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE TERT minimal promoter sequence.
 XX
 XX TERT; telomerase reverse transcriptase; TF-8; TF-13; repressor;
 KW cardiovascular; osteopathic; virucide; transcription; promoter; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200290570-A2.
 PN
 XX
 XX 14-NOV-2002.
 PD
 XX
 XX 07-MAY-2002; 2002WO-US014720.
 PF
 XX
 XX 08-MAY-2001; 2001US-0289717P.
 PR
 XX
 XX (SIERRA) SIERRA SCI INC.
 PA
 XX
 XX Andrews WH;
 PI
 XX WPI; 2003-103520/09.
 DR
 XX
 XX New telomerase reverse transcriptase (TERT) TF-8 and/or TF-13 repressor
 PT binding site, useful in regulating TERT expression and for screening
 PT agents that modulate TERT transcription repressing activity of the TF-8
 PT and TF-13 sites.
 XX
 PS Example; Page 28; 40pp; English.
 XX
 CC The invention relates to a new telomerase reverse transcriptase (TERT) TF
 -8 and/or TF-13 repressor binding site. The nucleic acid comprising the
 CC binding site sequence is useful in preparing constructs, such as vectors
 CC and expression systems, and probes for the TERT TF-8 and/or TF-13
 CC repressor binding site in non-human animals. Modulating the transcription
 CC repressing activity of TERT TF-8 and/or TF-13 repressor factors to
 CC regulate telomerase expression, can be used in immortalization of cells,
 CC production of reagents useful in life science research, and therapeutic
 CC research. Inhibitors of TERT transcription repression by a TF-8 and/or TF
 -13 repressor may be used for increasing the proliferative capacity of a
 CC cell, and for treating Progeria, Hutchinson-Gilford syndrome,
 CC cardiovascular disease, osteoporosis, or AIDS. The present sequence
 CC represents the TERT minimal promoter
 XX
 SQ Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
 Query Match 100.0%; Score 245; DB 8; Length 295;
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGCT 60
 |||||
 Db 36 CCCCACGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCGCCCTTCCAGCT 95

QY 61 CCGCTCTCCGCGGAGCCCGCCCGTCCGACCCCTCCGCGTCCCGGCCAGGCC 120
 DB 96 CCGCTCTCCGCGGAGCCCGCCCGTCCGACCCCTCCGCGTCCCGGCCAGGCC 155
 QY 121 CTTCCGGGCGCTCCAGCCCGTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGGGG 180
 DB 156 CTTCCGGGCGCTCCAGCCCGTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGGGG 215
 QY 181 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGCGGAGCCCTGCGGCCAGGCC 240
 DB 216 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGCGGAGCCCTGCGGCCAGGCC 275
 QY 241 CCGCG 245
 DB 276 CCGCG 280

RESULT 5
 ABZ23897
 ID ABZ23897 standard; DNA; 295 BP.
 AC ABZ23897;
 DT 18-MAR-2003 (first entry)
 XX TERT minimal promoter fragment.
 DE TERT; telomerase reverse transcriptase; promoter; cytostatic; anti-HIV;
 KW osteopathic; dermatological; gene therapy; transcription factor; TF;
 KW cardiant; human; da.
 OS Homo sapiens.
 XX WO200290571-A2.
 PN 14-NOV-2002.
 PD 07-MAY-2002; 2002WO-US014740.
 PF 08-MAY-2001; 2001US-0289641P.
 PR (SIERRA) SIERRA SCI INC.
 XX Andrews WH;
 PI WPI; 2003-120554/11.
 DR New nucleic acid having a nucleotide sequence that is identical to a
 PT telomerase reverse transcriptase (TERT) activator-binding site in the
 PT minimal TERT promoter useful for treating cellular proliferative
 PT diseases, e.g. cancer, AIDS.
 XX Example; Page 45; 60pp; English.
 PS The invention relates to a nucleic acid present in other than its natural
 CC environment, having a nucleotide sequence that is the same or is
 CC substantially identical to a telomerase reverse transcriptase (TERT)
 CC activator binding site in the minimal TERT promoter. The nucleic acids,
 CC agents and methods are useful for treating cellular proliferative
 CC diseases, e.g. cancer, acquired immunodeficiency syndrome (AIDS),
 CC cardiovascular diseases, or osteoporosis. They are also useful in immune
 CC senescence and skin rejuvenation. The nucleic acids are also useful in
 CC preparing constructs, e.g. vectors, expression systems, or probes. The
 CC present sequence represents the TERT minimal promoter
 XX Sequence 295 BP; 26 A; 147 C; 81 G; 41 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 245; DB 10; Length 295;
 Best Local Similarity 100.0%; Pred. No. 4.3e-34;
 Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 60

DB 36 CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTGCGCCCTTCCAGCT 95
 QY 61 CCGCTCTCCGCGGAGCCCGCCCGTCCGACCCCTCCGCGTCCCGGCCAGGCC 120
 DB 96 CCGCTCTCCGCGGAGCCCGCCCGTCCGACCCCTCCGCGTCCCGGCCAGGCC 155
 QY 121 CTTCCGGGCGCTCCAGCCCGTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGGGG 180
 DB 156 CTTCCGGGCGCTCCAGCCCGTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGGGG 215
 QY 181 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGCGGAGCCCTGCGGCCAGGCC 240
 DB 216 CGAGTTTCAGGACGCTGCTGCTGCGACGCTGCGGAGCCCTGCGGCCAGGCC 275
 QY 241 CCGCG 245
 DB 276 CCGCG 280

RESULT 6
 ADI33422
 ID ADI33422 standard; DNA; 455 BP.
 AC ADI33422;
 DT 22-APR-2004 (first entry)
 XX Human telomerase promoter (hTERT) DNA SeqID 4.
 DE human telomerase promoter; human; E1A; IRES; E1B; anticancer;
 KW cell death; cancer; cytostatic; da.
 OS Homo sapiens.
 XX WO2004005511-A1.
 PN 15-JAN-2004.
 PD 07-JUL-2003; 2003WO-JP008573.
 PF 08-JUL-2002; 2002JP-00198941.
 PR (KANS-) KANSAI TECHNOLOGY LICENSING ORG CO LTD.
 XX (FUJI/) FUJIWARA T.
 PA (TANA/) TANAKA N.
 PA (KYOS/) KYO S.
 XX Fujiwara T, Tanaka N, Kyo S, Shirakiya Y, Kawashima T;
 PI WPI; 2004-099391/10.
 DR Polynucleotide comprising a human telomerase promoter and an E1 gene for
 PT treating cancer.
 XX Example 1; SEQ ID NO 4; 34pp; Japanese.
 PS This invention relates to a novel polynucleotide comprising a human
 CC telomerase promoter and at least one viral E1 gene. Specifically, the E1
 CC genes are E1A, IRES and E1B and the human telomerase promoter is
 CC preferably hTERT. The present invention describes a virus containing this
 CC polynucleotide and an anticancer agent that replicates efficiently in
 CC tumour cells and causing cell death. As such, it can be used for the
 CC treatment of cancer, in particular cancer of the stomach, large
 CC intestine, lung, liver, prostate, pancreas, digestive tract, bladder,
 CC mammary gland, uterus, thyroid gland and ovary. Accordingly, this
 CC composition exhibits cytostatic activity. This polynucleotide sequence is
 CC the human telomerase promoter (hTERT) DNA of the invention.
 XX Sequence 455 BP; 41 A; 212 C; 142 G; 60 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 245; DB 12; Length 455;
 Best Local Similarity 100.0%; Pred. No. 4.1e-34;


```
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACAGTGGGAGGAGACTGGGACCCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 60
Db 211 CCCACAGTGGGAGGAGACTGGGACCCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 270
QY 61 CCGCTCTCCGCGGGAGCCGCGCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db 271 CCGCTCTCCGCGGGAGCCGCGCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 330
QY 121 CTTCCGGGCGCTCCAGAGCCCTTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGCGCG 180
Db 331 CTTCCGGGCGCTCCAGAGCCCTTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGCGCG 390
QY 181 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAGAGCCCTGCGCCCGGCCAGCC 240
Db 391 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAGAGCCCTGCGCCCGGCCAGCC 450
QY 241 CCGCG 245
Db 451 CCGCG 455

RESULT 7
ABS98580/c
ID ABS98580 standard; DNA; 955 BP.
XX
AC ABS98580;
XX
DT 29-AUG-2003 (revised)
DT 17-DEC-2002 (first entry)
XX
DE Ar17pA2fTtrtex right end viral DNA sequence.
XX
KW Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
KW inverted terminal repeat; ITR; termination signal sequence; lung cancer;
KW E2F responsive promoter; adenoviral packaging signal; prostate cancer;
KW neoplastic condition; colon cancer; cytostatic; immunostimulant;
KW gene therapy; ds.
XX
OS Viruses.
XX
PN WO200267861-A2.
XX
PD 06-SEP-2002.
XX
PF 22-FEB-2002; 2002WO-US005300.
XX
PR 23-FEB-2001; 2001US-0270922P.
PR 01-JUN-2001; 2001US-0295037P.
PR 14-JAN-2002; 2002US-0348670P.
XX
PA (NOVS ) NOVARTIS PHARMA AG.
XX
PI Enlist DL, Porry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM;
PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;
PI Police SR, Clarke L, Phipps S, Cheng C;
XX
DR WPI; 2002-706950/76.
XX
PT Recombinant viral vector comprising an adenoviral nucleic acid backbone,
PT useful for treating neoplastic disorders such as lung, breast, prostate
PT or colon cancer.
XX
PS Example 15; Fig 47; 226pp; English.
XX
CC The present invention relates to a new recombinant viral vector
CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E2F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. the methods and
CC compositions of the present invention are useful for treating a
```

```
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a viral DNA sequence that was used in the methods of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 955 BP; 266 A; 286 C; 236 G; 167 T; 0 U; 0 Other;
Query Match 100.0%; Score 245; DB 6; Length 955;
Best Local Similarity 100.0%; Pred. No. 3.6e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCACAGTGGGAGGAGACTGGGACCCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 60
Db 500 CCCACAGTGGGAGGAGACTGGGACCCGGGACCCGTCCTGCCCCCTTACCTTCCAGCT 441
QY 61 CCGCTCTCTCCGCGGGAGCCGCGCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db 440 CCGCTCTCTCCGCGGGAGCCGCGCCGCTCCGACCCCTCCGGGTCCCGGCCAGGCC 381
QY 121 CTTCCGGGCGCTCCAGAGCCCTTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGCGCG 180
Db 380 CTTCCGGGCGCTCCAGAGCCCTTCCCTTCTTCCGCGGCGCCCGCCCTCTCTCGCGCG 321
QY 181 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAGAGCCCTGCGCCCGGCCAGCC 240
Db 320 CGAGTTTCAGGAGCGCTGCGTCTGCTGCGCACTGGGAGAGCCCTGCGCCCGGCCAGCC 261
QY 241 CCGCG 245
Db 260 CCGCG 256

RESULT 8
AAX88272
ID AAX88272 standard; DNA; 5126 BP.
XX
AC AAX88272;
XX
DT 22-SEP-1999 (first entry)
XX
DE Human catalytic telomerase subunit 5'-flanking regulatory DNA.
XX
KW Telomerase; subunit; human; regulatory; catalytic; anti-tumour; reporter;
KW modulator; telomerase regulatory region; cancer therapy; ss.
XX
OS Homo sapiens.
XX
PN DE19757984-A1.
XX
PD 01-JUL-1999.
XX
PF 24-DEC-1997; 97DE-01057984.
XX
PR 24-DEC-1997; 97DE-01057984.
XX
PA (FARB ) BAYER AG.
XX
PI Hagen G, Wick M, Zubov D;
XX
DR WPI; 1999-372320/32.
XX
PT New 5' flanking regulatory sequence from the human catalytic telomerase
PT subunit gene useful for cancer therapy.
XX
PS Claim 1; Fig 4; 14pp; German.
XX
CC This invention describes a novel 5' flanking regulatory sequence from the
CC human catalytic telomerase subunit gene. Recombinant constructs
CC containing the product of the invention can be linked with DNA encoding
CC an anti-tumour protein or reporter protein. The constructs are useful for
CC identifying candidate substances that modulate the activity of the
CC telomerase regulatory region. The constructs can be used in cancer
```

```
CC therapy
XX Sequence 5126 BP; 1009 A; 1532 C; 1404 G; 1180 T; 0 U; 1 Other;
SQ Query Match 100.0%; Score 245; DB 2; Length 5126;
Best Local Similarity 100.0%; Pred. No. 2.8e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGGAGGACTGGGGACCCCGGACCGTCTCCCTTCCAGCTTCCAGCT 60
DB 4879 CCCCAGTGGCGGAGGACTGGGGACCCCGGACCGTCTCCCTTCCAGCTTCCAGCT 4938

QY 61 CGGCTCTCTCCGCGGAGACCCCGCCCGTCCGACACCCCTCCCGGGTCCCGGCCAGGCC 120
DB 4939 CGGCTCTCTCCGCGGAGACCCCGCCCGTCCGACACCCCTCCCGGGTCCCGGCCAGGCC 4998

QY 121 CTTCCGGGCGCTTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCTCTCTCTCGGGGG 180
DB 4999 CTTCCGGGCGCTTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCTCTCTCTCGGGGG 5058

QY 181 CGAGTTTCAGGACGCTGGTCTCTGCGCACGTTGGGAGCCCTGGCCCGGCCACCC 240
DB 5059 CGAGTTTCAGGACGCTGGTCTCTGCGCACGTTGGGAGCCCTGGCCCGGCCACCC 5118

QY 241 CCGCG 245
DB 5119 CCGCG 5123

RESULT 9
ID ABK12707 standard; DNA; 5928 BP.
AC ABK12707;
XX 18-JUN-2002 (first entry)
XX Minimal telomerase promoter in plasmid designated pSSI20.
XX Human; telomerase reverse transcriptase; TERT; Site C; Progeria; burn;
KW repressor binding site; Hutchinson-Gilford syndrome; AIDS; cancer;
KW acquired immunodeficiency syndrome; cardiovascular disease; osteoporosis;
KW skin rejuvenation; immune senescence; bone marrow transplant; skin graft;
KW neoplastic disease; TERT minimal promoter; plasmid pSSI20; ss.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FH misc_feature 38..295
FT /*tag= a
FT /*note= "Telomerase minimal promoter"
FT misc_feature 295..310
FT /*tag= b
FT /*note= "Kozak fragment"
FT misc_feature 308..1864
FT /*tag= c
FT /*note= "Secreted Alkaline Phosphatase gene"
FT polyA_site 1860..2080
FT /*tag= d
FT /*standard_name= "PolyA addition site"
FT /*note= "Late Poly-A addition site of SV40"
FT misc_feature 2394..2976
FT /*tag= e
FT /*note= "Bacterial origin of replication"
FT misc_feature 3170..4023
FT /*tag= f
FT /*note= "Ampicillin Resistance Gene, made sensitive by mutagenesis"
FT misc_feature 4538..5196
FT /*tag= g
FT /*note= "Chloramphenicol Resistance Gene"
FT
```

```
FT misc_feature 5217..5401
FT /*tag= h
FT /*note= "F1 Origin of Replication"
FT misc_feature 5768..5921
FT /*tag= i
FT /*note= "Transcription blocker"
XX WO200216657-A1.
PN 28-FEB-2002.
XX 17-AUG-2001; 2001WO-US025861.
XX 24-AUG-2000; 2000US-0227865P.
PR 01-SEP-2000; 2000US-0230174P.
PR 05-OCT-2000; 2000US-0238345P.
XX (STER-) SIERRA SCI INC.
XX Andrews WH, Foster CA, Fraser S, Mohammadpour H;
PI MPI; 2002-280952/32.
XX Modulating expression of telomerase reverse transcriptase (TERT) in a cell, for regulating proliferative capacity of a cell, involves modulating TERT transcription repression by Site C repressor binding site.
XX Disclosure; Fig 2; 66pp; English.
XX The present invention relates to a new method of modulating expression of telomerase reverse transcriptase (TERT) from a TERT expression system that includes a TERT promoter and a Site C repressor binding site. The method of the invention involves modulating TERT transcription repression by the Site C repressor binding site. The method of the invention is useful for modulating expression of TERT for producing a mammalian antibody. The method is also useful in a variety of different applications, including immortalisation of cells, production of reagents for use in life science research, therapeutic applications, and therapeutic agent screening applications. Increasing TERT expression delays natural telomeric shortening and/or increases telomeric length and is useful for treating disease conditions such as Progeria or Hutchinson-Gilford syndrome, acquired immunodeficiency syndrome (AIDS), cardiovascular disease, osteoporosis, in skin rejuvenation and to inhibit immune senescence. The method can be employed to lengthen telomeres of osteoblast and osteoclast stem cells, encouraging bone replacement and proper remodeling and reinforcement, and can thus be used in bone marrow transplants for the treatment of cancer and skin grafts for burn victims and as such the method improves the survival and effectiveness of bone marrow and skin cell transplants. Decreasing TERT expression is useful for treating cellular proliferative disease conditions, including cancer, neoplastic disease conditions e.g. cancer. The present nucleic acid sequence represents plasmid SSI20 minimal telomerase promoter sequence. This sequence contains part of the human TERT minimal promoter sequence (ABK12706)
```

Sequence 5928 BP; 1445 A; 1607 C; 1541 G; 1335 T; 0 U; 0 Other;

```
Query Match 100.0%; Score 245; DB 6; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.7e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGGAGGACTGGGGACCCCGGACCGTCTCGCCCTTCCAGCTTCCAGCT 60
DB 51 CCCCAGTGGCGGAGGACTGGGGACCCCGGACCGTCTCGCCCTTCCAGCTTCCAGCT 110

QY 61 CGGCTCTCTCCGCGGAGACCCCGCCCGTCCGACACCCCTCCGGGTCCCGGCCAGGCC 120
DB 111 CGGCTCTCTCCGCGGAGACCCCGCCCGTCCGACACCCCTCCCGGTCCCGGCCAGGCC 170

QY 121 CTTCCGGGCGCTTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCTCTCTCTCGGGGG 180
DB 171 CTTCCGGGCGCTTCCAGCCCTTCCCTTCTTTCGCGGCGCCCGCTCTCTCTCGGGGG 230
```

```
Oy 181 CGAGTTTCAGCGAGCGCTGCGTCTGCTGCGCACCTGGGAAGCCCTGCCCGCGCCACCC 240
    |||||
Db 231 CGAGTTTCAGCGAGCGCTGCGTCTGCTGCGCACCTGGGAAGCCCTGCCCGCGCCACCC 290
    |||||
Oy 241 CCGCG 245
    |||||
Db 291 CCGCG 295
    |||||

RESULT 10
AAS96607
ID AAS96607 standard; DNA; 51552 BP.
XX AC
XX AC
XX AC
XX AC
XX 09-APR-2002 (first entry)
XX DNA encoding human telomerase reverse transcriptase (TERT) #1.
XX Telomerase reverse transcriptase; TERT; cytosolic; apoptosis;
KW cell growth inhibitor; antisense oligonucleotide; antisense technology;
KW ds.
XX Homo sapiens.
XX Key
FH Location/Qualifiers
FT 1..11492
FT exon /*tag= a
FT number= 1
FT 11274..47813
FT /*tag= b
FT /*product= "TERT"
FT /*note= "Telomerase reverse transcriptase"
FT 11493..11596
FT /*tag= c
FT number= 1
FT 11597..12950
FT /*tag= d
FT number= 2
FT 12951..21566
FT /*tag= e
FT number= 2
FT 21567..21762
FT /*tag= f
FT number= 3
FT 21763..23851
FT /*tag= g
FT number= 3
FT 23852..24032
FT /*tag= h
FT number= 4
FT 24033..24719
FT /*tag= i
FT number= 4
FT 24720..24899
FT /*tag= j
FT number= 5
FT 24900..25393
FT /*tag= k
FT number= 5
FT 25394..25549
FT /*tag= l
FT number= 6
FT 25550..30195
FT /*tag= m
FT number= 6
FT 30196..30292
FT /*tag= n
FT number= 7
FT 30293..31272
FT /*tag= o
FT number= 7
FT 31273..31358
FT /*tag= p
FT number= 8
FT 31359..33843
FT /*tag= q
FT number= 8
FT 33844..33957
FT /*tag= r
FT number= 9
FT 33958..35941
FT /*tag= s
FT number= 9
FT 35942..36013
FT /*tag= t
FT number= 10
FT 36014..37884
FT /*tag= u
FT number= 10
FT 37885..38073
FT /*tag= v
FT number= 11
FT 38074..41874
FT /*tag= w
FT number= 11
FT 41875..42001
FT /*tag= x
FT number= 12
FT 42002..42881
FT /*tag= y
FT number= 12
FT 42882..42943
FT /*tag= z
FT number= 13
FT 42944..46129
FT /*tag= aa
FT number= 13
FT 46130..46254
FT /*tag= ab
FT number= 14
FT 46255..47035
FT /*tag= ac
FT number= 14
FT 47036..47173
FT /*tag= ad
FT number= 15
FT 47174..47709
FT /*tag= ae
FT number= 15
FT 47710..50544
FT /*tag= af
FT number= 16
XX WO200188198-A1.
XX
XX 22-NOV-2001.
XX
XX 15-MAY-2001; 2001WO-US015774.
XX
XX 16-MAY-2000; 2000US-00572423.
XX 07-DEC-2000; 2000US-00733294.
XX
XX (ISIS-) ISIS PHARM INC.
XX Monia BP, Gaarde WA, Freier SM, Wancewicz E;
XX WPI; 2002-075321/10.
DR P-PSDB; AAU72735.
XX
XX New compound targeted to nucleic acid molecule encoding telomerase
PT transcriptase (TERT), which specifically hybridizes with and inhibits
PT expression of TERT, useful for modulating apoptosis and inhibiting cell
PT growth.
XX
```

```
PS Example 19; Page 112-138; 154pp; English.
XX
CC The invention describes a compound, 8-50 nucleobases in length targeted
CC to a nucleic acid molecule encoding human TERT (telomerase reverse
CC transcriptase), where the compound specifically hybridizes with and
CC inhibits the expression of TERT. A series of oligonucleotides were
CC designed to target different regions of the human TERT RNA. These were 20
CC nucleotides in length and composed of a central gap region consisting of
CC ten 2'-deoxynucleotides, flanked on both sides (5' and 3' directions) by
CC five-nucleotide wings. The wings were composed of 2'-methoxyethyl (2'-
CC MOE) nucleotides. The compounds were analysed for their effect on human
CC TERT mRNA levels by reverse transcriptase (RT)-polymerase chain reaction
CC (PCR). The compound is useful for inhibiting the expression of TERT in
CC cells or tissues, for treating a human having disease or condition
CC associated with TERT, for modulating apoptosis, for inhibiting cell
CC growth (preferably, cancer cell growth), in antisense therapy and for
CC diagnostics and therapeutics. This sequence encodes human telomerase
CC reverse transcriptase (TERT) #1, and is used to create antisense
CC oligonucleotides which modify TERT expression, described in the method of
CC the invention
XX
SQ Sequence 51552 BP; 10709 A; 13313 C; 15370 G; 12158 T; 0 U; 2 Other;
Query Match 100.0%; Score 245; DB 6; Length 51552;
Best Local Similarity 100.0%; Pred. No. 1.9e-34;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCCACCTTCCAGCT 60
DB 11029 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCCACCTTCCAGCT 11088
QY 61 CCGCCTCTCTCCGCGCGGACCCCGCCCGGTCGCCAGCCCTCCGGGTCGCCGCGCCAGCCC 120
DB 11089 CCGCCTCTCTCCGCGCGGACCCCGCCCGGTCGCCAGCCCTCCGGGTCGCCGCGCCAGCCC 11148
QY 121 CTTCCGGGCGCTCCAGCCCGCTCCCTTCTGTCGGGCGCCCGCCCTCTCTCCGGGCG 180
DB 11149 CTTCCGGGCGCTCCAGCCCGCTCCCTTCTGTCGGGCGCCCGCCCTCTCTCCGGGCG 11208
QY 181 CGAGTTTCAGGACGCTGGTCTCTGTCGGGACGCTGGGAAGCCCTGGCCCGCCAGCCC 240
DB 11209 CGAGTTTCAGGACGCTGGTCTCTGTCGGGACGCTGGGAGCCCTGGCCCGCCAGCCC 11268
QY 241 CCGCG 245
DB 11269 CCGCG 11273
RESULT 11
ACC47272
XX ACC47272 standard; DNA; 378 BP.
XX
AC ACC47272;
XX
XX 11-AUG-2003 (first entry)
XX CEA gene cis-acting sequence.
XX
XX Gene expression; promoter; cytostatic; gene therapy; antisense therapy;
XX cancer; cis-acting; CEA gene; ds.
XX
XX Unidentified.
XX
XX WO2003013555-A1.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-US024741.
XX
XX 08-AUG-2001; 2001US-0310905P.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Fang B;
XX
DR WPI; 2003-256488/25.
XX
PT Expressing gene products in a cell type-preferential manner with a binary
PT or bicistronic expression system, useful for treating cancers of the
PT brain, head and neck, esophagus, thyroid, stomach, colon, liver,
PT prostate, skin and rectum.
XX
PS Disclosure; Page 139; 141pp; English.
XX
CC The invention relates to expressing gene product in a cell type-
CC preferential manner. The method involves providing a first expression
CC cassette having a cell type-preferential promoter, providing a second
CC expression cassette having an inducible promoter, and transferring the
CC first and second expression cassettes into a cell in which the cell type
CC -specific preferential promoter is active. The methods and compositions
CC of the present invention are useful for treating cancers of the brain,
CC head and neck, esophagus, thyroid, stomach, colon, liver, kidney,
CC prostate, breast, cervix, ovaries, testicles, rectum, skin and blood. The
CC present sequence represents a cis-acting sequence that confers expression
CC of the CEA gene
XX
SQ Sequence 378 BP; 35 A; 178 C; 121 G; 44 T; 0 U; 0 Other;
Query Match 99.6%; Score 244; DB 8; Length 378;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCCACCTTCCAGCT 60
DB 135 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGTCCTGCCCCCTTCCACCTTCCAGCT 194
QY 61 CCGCCTCTCTCCGCGCGGACCCCGCCCGGTCGCCAGCCCTCCGGGTCGCCGCGCCAGCCC 120
DB 195 CCGCCTCTCTCCGCGCGGACCCCGCCCGGTCGCCAGCCCTCCGGGTCGCCGCGCCAGCCC 254
QY 121 CTTCCGGGCGCTCCAGCCCGCTCCCTTCTGTCGGGCGCCCGCCCTCTCTCCGGGCG 180
DB 255 CTTCCGGGCGCTCCAGCCCGCTCCCTTCTGTCGGGCGCCCGCCCTCTCTCCGGGCG 314
QY 181 CGAGTTTCAGGACGCTGGTCTCTGTCGGGACGCTGGGAAGCCCTGGCCCGCCAGCCC 240
DB 315 CGAGTTTCAGGACGCTGGTCTCTGTCGGGACGCTGGGAGCCCTGGCCCGCCAGCCC 374
QY 241 CCGCG 244
DB 375 CCGCG 378
RESULT 12
ABS98658
ID ABS98658 standard; DNA; 397 BP.
XX
XX ABS98658;
XX
XX 17-DEC-2002 (first entry)
XX Human TERT promoter sequence #1.
XX
XX Virus; viral vector; adenoviral nucleic acid backbone; breast cancer;
XX inverted terminal repeat; ITR; termination signal sequence; lung cancer;
XX E2F responsive promoter; adenoviral packaging signal; prostate cancer;
XX neoplastic condition; colon cancer; cytostatic; immunostimulant;
XX gene therapy; human; TERT; promoter; ds.
XX
XX Homo sapiens.
XX
XX WO200267861-A2.
XX
XX 06-SEP-2002.
XX
XX 22-FEB-2002; 2002WO-US005300.
XX
```

```
XX 23-FEB-2001; 2001US-0270922P.
PR 01-JUN-2001; 2001US-0295037P.
PR 14-JAN-2002; 2002US-0348670P.
XX (NOVS ) NOVARTIS PHARMA AG.
XX Ennist DL, Forry-Schaudies S, Gorziglia M, Hallenbeck PL, Hay CM;
PI Jakubczak JL, Kaleko M, Ryan PC, Stewart DA, Xie Y, Connelly S;
PI Police SR, Clarke L, Phipps S, Cheng C;
XX WPI; 2002-706950/76.
XX Recombinant viral vector comprising an adenoviral nucleic acid backbone,
PT useful for treating neoplastic disorders such as lung, breast, prostate
PT or colon cancer.
XX Claim 11; Page 21; 226pp; English.
XX The present invention relates to a new recombinant viral vector
CC comprising an adenoviral nucleic acid backbone, where the backbone
CC comprises in sequential order, a left inverted terminal repeat (ITR), a
CC termination signal sequence, an E3F responsive promoter which is operably
CC linked to a gene essential for replication of the recombinant viral
CC vector, an adenoviral packaging signal and a right ITR. The methods and
CC compositions of the present invention are useful for treating a
CC neoplastic condition such as lung, breast, prostate or colon cancer. The
CC viral vectors are useful in studying methods of killing neoplastic cells
CC in vitro or in animal models. The present nucleic acid sequence
CC represents a human TERT promoter of the invention
XX Sequence 397 BP; 35 A; 186 C; 127 G; 49 T; 0 U; 0 Other;
SQ Query Match 99.6%; Score 244; DB 6; Length 397;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGAGGAGTGGGACCCCGGGACCCCGTCTGCCCCCTTCCAGTTC 61
DB 154 CCCACGTGGCGAGGAGTGGGACCCCGGGACCCCGTCTGCCCCCTTCCAGTTC 213
QY 62 CGCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGTCCCGGCCAGCCCC 121
DB 214 CGCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTCCCGGTCCCGGCCAGCCCC 273
QY 122 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGCGGCCCGCCCTCTCTCTCGGGGCGC 181
DB 274 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGCGGCCCGCCCTCTCTCTCGGGGCGC 333
QY 182 GAGTTTCAGGCAGCGCTGCTCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 241
DB 334 GAGTTTCAGGCAGCGCTGCTCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 393
QY 242 CGCG 245
DB 394 CGCG 397
RESULT 13
ADR73423
ID ADR73423 standard; DNA; 408 BP.
XX ADR73423;
XX ADR73423;
XX 02-DEC-2004 (first entry)
XX Human telomerase reverse transcriptase (hTERT) gene promoter sequence.
DE ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
KW c-Myc binding site; Sp1 binding site; cancer.
XX Homo sapiens.
OS
```

```
XX WO2004076668-A1.
XX 10-SEP-2004.
XX 27-FEB-2004; 2004WO-KR000427.
XX 27-FEB-2003; 2003KR-00012364.
XX (YUNC/) YUN C.
XX (KIMJ/) KIM J.
XX Yun C, Kim J, Yang J;
XX WPI; 2004-653423/63.
XX New transcriptional regulatory sequence with a human telomere reverse
PT transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
PT ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
PT head and neck cancer.
XX Disclosure; SEQ ID NO 1; 130pp; English.
XX The invention relates to a transcriptional regulatory sequence with a
CC human telomere reverse transcriptase (hTERT) promoter linked to a
CC nucleotide sequence comprising one or more c-Myc binding sites and/or one
CC or more Sp1 binding sites. The transcriptional regulatory sequence and
CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
CC colon, cervical, breast, brain, or head and neck cancer. This sequence
CC corresponds to the wild type human telomerase reverse transcriptase
CC (hTERT) promoter sequence used to generate the novel sequence of the
CC invention.
XX Sequence 408 BP; 35 A; 190 C; 132 G; 51 T; 0 U; 0 Other;
SQ Query Match 99.6%; Score 244; DB 13; Length 408;
Best Local Similarity 100.0%; Pred. No. 6.2e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGAGGAGTGGGACCCCGGGACCCCGTCTGCCCCCTTCCAGTTC 61
DB 165 CCCACGTGGCGAGGAGTGGGACCCCGGGACCCCGTCTGCCCCCTTCCAGTTC 224
QY 62 CGCTCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 121
DB 225 CGCTCTCTCCCGCGGAGCCCGCCCGTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 284
QY 122 CTCGGGGCCCTCCAGCCCTTCCCTTTCGCGGCCCGCCCTCTCTCTCGGGGCGC 181
DB 285 CTCGGGGCCCTCCAGCCCTTCCCTTTCGCGGCCCGCCCTCTCTCTCGGGGCGC 344
QY 182 GAGTTTCAGGCAGCGCTGCTCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 241
DB 345 GAGTTTCAGGCAGCGCTGCTCTGCGCACGCTGGGAAGCCCTTGGCCCGGCCACCCC 404
QY 242 CGCG 245
DB 405 CGCG 408
RESULT 14
ADR73427
ID ADR73427 standard; DNA; 902 BP.
XX ADR73427;
XX ADR73427;
XX 02-DEC-2004 (first entry)
XX Human m-hTERT gene promoter sequence.
DE ds; cytosstatic; gene therapy; transcriptional regulatory sequence;
KW human telomere reverse transcriptase; hTERT; promoter;
KW
```

CC c-Myc binding site; Sp1 binding site; cancer.
CC Homo sapiens.
XX Key
FH Location/Qualifiers
FT protein_bind 173..178
FT /tag= a
FT /bound_moiety= "c-Myc protein"
FT 228..236
FT /tag= b
FT /bound_moiety= "Sp1 transcription factor"
FT 250..255
FT /tag= c
FT /bound_moiety= "Sp1 transcription factor"
FT 282..290
FT /tag= d
FT /bound_moiety= "Sp1 transcription factor"
FT 302..310
FT /tag= e
FT /bound_moiety= "Sp1 transcription factor"
FT 311..336
FT /tag= f
FT /bound_moiety= "Sp1 transcription factor"
FT 381..386
FT /tag= g
FT /bound_moiety= "c-Myc protein"
FT 617..622
FT /tag= h
FT /bound_moiety= "c-Myc protein"
FT 672..680
FT /tag= i
FT /bound_moiety= "Sp1 transcription factor"
FT 694..699
FT /tag= j
FT /bound_moiety= "Sp1 transcription factor"
FT 726..734
FT /tag= k
FT /bound_moiety= "Sp1 transcription factor"
FT 746..754
FT /tag= l
FT /bound_moiety= "Sp1 transcription factor"
FT 775..780
FT /tag= m
FT /bound_moiety= "Sp1 transcription factor"
FT 900
FT /tag= n
FT /note= "translation start site"

XX WO2004076668-A1.
XX 10-SEP-2004.
XX 27-FEB-2004; 2004WO-KR000427.
XX 27-FEB-2003; 2003KR-00012364.
XX (YUNC/) YUN C.
XX (KIMJ/) KIM J.
XX Yun C, Kim J, Yang J;
XX WPI; 2004-653423/63.
XX New transcriptional regulatory sequence with a human telomere reverse
XX transcriptase promoter, useful for treating cancer, e.g. stomach, lung,
XX ovarian, liver, pancreatic, bladder, colon, cervical, breast, brain, or
XX head and neck cancer.

XX Claim 6; SEQ ID NO 13; 130pp; English.
XX PS
XX This invention relates to a transcriptional regulatory sequence with a
XX human telomere reverse transcriptase (hTERT) promoter linked to a
XX nucleotide sequence comprising one or more c-Myc binding sites and/or one

CC or more Sp1 binding sites. The transcriptional regulatory sequence and
CC composition are useful for treating cancer, e.g. stomach, lung, ovarian,
CC liver, bronchogenic, nasopharyngeal, laryngeal, pancreatic, bladder,
CC colon, cervical, breast, brain, or head and neck cancer. This sequence
CC corresponds to the modified human telomerase reverse transcriptase
CC (hTERT) promoter sequence containing the extra c-Myc and Sp1 binding site
CC sequences.

XX SQ Sequence 902 BP; 103 A; 388 C; 282 G; 129 T; 0 U; 0 Other;

Query Match 99.6%; Score 244; DB 13; Length 902;
Best Local Similarity 100.0%; Pred. No. 5.4e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCACGTGCGGAGGAGTCTGGGGACCCGGGACCCGTCCTCTCCCTTCACTTCAGGTC 61
DB 171 CCCACGTGCGGAGGAGTCTGGGGACCCGGGACCCGTCCTCTCCCTTCACTTCAGGTC 230
QY 62 GCCTCTCTCGGGGACCCGCGTCCGACCCCTCCGGGTCCCGGCCCGGCCCGCC 121
DB 231 GCCTCTCTCGGGGACCCGCGTCCGACCCCTCCGGGTCCCGGCCCGGCCCGCC 290
QY 122 CTCGGGCGCTCCCGACCCCTCCCTTCTTTCGGGGCGCCCGCTCTCTCTCGGGGCG 181
DB 291 CTCGGGCGCTCCCGACCCCTCCCTTCTTTCGGGGCGCCCGCTCTCTCTCGGGGCG 350
QY 182 GAGTTTCAGGAGCGCTCGTCTGTCGCGACGTCGCGGAGGAGCCCTGGGCCCGCCCGCC 241
DB 351 GAGTTTCAGGAGCGCTCGTCTGTCGCGACGTCGCGGAGGAGCCCTGGGCCCGCCCGCC 410
QY 242 CGCG 245
DB 411 CGCG 414

RESULT 15
AAH41091
ID AAH41091 standard; DNA; 3962 BP.
XX AC AAH41091;
XX 29-AUG-2001 (first entry)
DT Telomerase reverse transcriptase (TERT) DNA.
DE Phenotype switch molecule; phenotype-related gene battery;
XX gene localisation; telomere reverse transcriptase; TERT; ds.
KW Unidentified.
XX OS
XX WO200138515-A1.
XX 31-MAY-2001.
XX 17-NOV-2000; 2000WO-CN000427.
XX 19-NOV-1999; 99CN-00121466.
XX (BIAN/) BIAN X.
XX BIAN X;
XX WPI; 2001-367684/38.
XX Isolating phenotype switch molecules and phenotype-related gene batteries
XX from complex genomes of higher animals and plants, useful e.g. in gene
XX localization and classification analysis.

XX Example 7; Page 27-29; 35pp; Chinese.
XX This invention relates to a method for isolating phenotype switch
XX molecules and phenotype-related gene batteries from complex genomes of
XX higher animals and plants. The method is useful in gene localisation and

CC classification analysis, studying gene development networks and function
CC networks, and designing drugs based on regulatory sequences of the
CC phenotypes for disease treatment. The present sequence represents DNA
CC encoding a telomere reverse transcriptase (TERT), which is used in an
CC example illustrating the use of the method of the invention
XX
SQ Sequence 3962 BP; 782 A; 1157 C; 1113 G; 910 T; 0 U; 0 Other;

Query Match 99.6%; Score 244; DB 4; Length 3962;
Best Local Similarity 100.0%; Pred. No. 4.3e-34;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CCCACGTGCGGAGGACTGGGGACCGGGACCCCGTCTGCTGCTTACCTTCAGCTC 61
Db 3682 CCCACGTGCGGAGGACTGGGGACCGGGACCCCGTCTGCTGCTTACCTTCAGCTC 3741
Qy 62 CGCCTCTCTCCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGCCAGCCCC 121
Db 3742 CGCCTCTCTCCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGCCAGCCCC 3801
Qy 122 CTCGGGCGCTTCCAGCCCTTCCCTTTCGCGGCCCGCCCTCTCTCGCGGCGC 181
Db 3802 CTCGGGCGCTTCCAGCCCTTCCCTTTCGCGGCCCGCCCTCTCTCGCGGCGC 3861
Qy 182 GAGTTTCAGGACGCGCTCGCTCTGCGACGTCGGAGCCCTGGGCCCGGCCACCCC 241
Db 3862 GAGTTTCAGGACGCGCTCGCTCTGCGACGTCGGAGCCCTGGGCCCGGCCACCCC 3921
Qy 242 CGCG 245
Db 3922 CGCG 3925

Search completed: April 9, 2005, 06:08:13
Job time : 257.83 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:45:13 ; Search time 77.8505 Seconds
(without alignments)
5149.459 Million cell updates/sec

Title: US-10-081-969-94

Perfect score: 245

Sequence: 1 cccacgtgcggaggagact.....tggcccccggccacccccgcg 245

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	261	US-09-932-581-24	Sequence 24, Appl
2	245	100.0	5928	US-09-932-581-25	Sequence 25, Appl
3	245	100.0	44952	US-09-949-016-12197	Sequence 12197, A
4	245	100.0	44960	US-09-949-016-17583	Sequence 17583, A
5	245	100.0	51552	US-09-733-294A-30	Sequence 30, Appl
6	244	99.6	298	US-09-244-438-17	Sequence 17, Appl
7	244	99.6	4321	US-09-402-181B-6	Sequence 6, Appl
8	244	99.6	15418	US-09-783-203-1	Sequence 1, Appl
9	244	99.6	15418	US-09-994-427A-1	Sequence 1, Appl
10	244	99.6	15418	US-09-244-438-1	Sequence 1, Appl
11	229.8	93.8	314	US-09-916-510A-8	Sequence 8, Appl
12	204.4	83.4	4200	US-08-913-951-6	Sequence 6, Appl
13	201.2	82.1	35871	US-09-956-335-2	Sequence 2, Appl
14	201.2	82.1	35978	US-09-956-335-1	Sequence 1, Appl
15	199.8	81.6	4335	US-08-974-549A-6	Sequence 6, Appl
16	199.8	81.6	4335	US-09-721-456-6	Sequence 6, Appl
17	198	80.8	1677	US-09-956-335-3	Sequence 3, Appl
18	93.6	38.2	124	US-08-974-549A-726	Sequence 726, App
19	93.6	38.2	124	US-09-721-456-726	Sequence 726, App
20	77	31.4	78	US-09-932-581-7	Sequence 7, Appl
21	74	30.2	77	US-09-244-438-19	Sequence 19, Appl
22	74	30.2	89	US-09-244-438-20	Sequence 20, Appl
23	65.2	26.6	319	US-09-165-264-8	Sequence 8, Appl
24	64.6	26.4	320	US-09-165-264-7	Sequence 7, Appl
25	63.4	25.9	865	US-09-270-767-11042	Sequence 11042, A
26	62.8	25.6	320	US-09-165-264-14	Sequence 14, Appl
27	62.2	25.4	320	US-09-165-264-13	Sequence 13, Appl

c	28	61.6	25.1	318	3	US-09-165-264-12	Sequence 12, Appl
c	29	61.2	25.0	320	3	US-09-165-264-11	Sequence 11, Appl
c	30	60	24.5	14340	4	US-09-949-016-16972	Sequence 16972, A
	31	58.8	24.0	7218	1	US-08-232-463-14	Sequence 14, Appl
	32	57.2	23.3	12001	1	US-08-458-568A-11	Sequence 11, Appl
	33	57.2	23.3	152331	3	US-09-128-155-16	Sequence 16, Appl
	34	55	22.4	3855	3	US-08-974-549A-4	Sequence 4, Appl
	35	55	22.4	3855	4	US-08-912-951-4	Sequence 4, Appl
	36	55	22.4	3855	4	US-09-402-181B-4	Sequence 4, Appl
	37	55	22.4	3855	4	US-09-721-456-4	Sequence 4, Appl
	38	55	22.4	4015	3	US-08-851-843A-224	Sequence 224, App
	39	55	22.4	4015	3	US-08-974-549A-1	Sequence 1, Appl
	40	55	22.4	4015	3	US-08-854-050-224	Sequence 224, App
	41	55	22.4	4015	3	US-09-430-323-224	Sequence 224, App
	42	55	22.4	4015	3	US-09-572-423B-3	Sequence 3, Appl
	43	55	22.4	4015	3	US-09-128-354-1	Sequence 1, Appl
	44	55	22.4	4015	3	US-09-675-321-1	Sequence 1, Appl
	45	55	22.4	4015	3	US-09-052-919-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-932-581-24

; Sequence 24, Application US/09932581

; Patent No. 6686159

; GENERAL INFORMATION:

; APPLICANT: Andrews, William H.

; APPLICANT: Foster, Christopher A.

; APPLICANT: Fraser, Stephanie

; APPLICANT: Mohammadpour, Hamid

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING

; FILE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION

; FILE REFERENCE: STER-005

; CURRENT APPLICATION NUMBER: US/09/932,581

; CURRENT FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: 60/227,865

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: 60/230,174

; PRIOR FILING DATE: 2000-09-01

; PRIOR APPLICATION NUMBER: 60/238,345

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24

; LENGTH: 261

; TYPE: DNA

; ORGANISM: human

US-09-932-581-24

Query Match 100.0%; Score 245; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.9e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGCGGAGGAGCTGGGACCCGGGACCCGCTCTGCTCCCTTCCAGCT 60

Db 14 CCCACGTGCGGAGGAGCTGGGACCCGGGACCCGCTCTGCTCCCTTCCAGCT 73

Qy 61 CGGCTCTCTCGCGGGAGCCCGCCCGCTCCGAGCCCTCCGCGGTCGCCGCCAGGCC 120

Db 74 CGGCTCTCTCGCGGGAGCCCGCCCGCTCCGAGCCCTCCGCGGTCGCCGCCAGGCC 133

Qy 121 CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 180

Db 134 CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGCGGGCCCGCCCTCTCTCTCGGGCG 193

Qy 181 CGAGTTTCAGGACGCTGCGTCTCTGTCGACGTGGGAGCCCTGCGCCCGGCCACCC 240

Db 194 CGAGTTTCAGGACGCTGCGTCTCTGTCGACGTGGGAGCCCTGCGCCCGGCCACCC 253

Qy 241 CGCG 245

|||||

```
Db      254 CCGCG 258

RESULT 2
US-09-932-581-25
; Sequence 25, Application US/09932581
; Patent No. 6686159
; GENERAL INFORMATION:
; APPLICANT: Andrews, Christopher A.
; APPLICANT: Posters, Stephanie
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932,581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
US-09-932-581-25

Query Match      100.0%; Score 245; DB 4; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.8e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 60
Db      51 CCCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 110

QY      61 CGCCTCTCCGCGCGGAGACCCGCCCGCTCCCGACCCCTCCGCGGTCGCCGCGACGCC 120
Db      111 CGCCTCTCCGCGCGGAGACCCGCCCGCTCCCGACCCCTCCGCGGTCGCCGCGACGCC 170

QY      121 CTTCCGGGCCCCCAGCCGCTCCCTTCTTCCGGGCCCCGCGCTCTCTCGGGCG 180
Db      171 CTTCCGGGCCCCCAGCCGCTCCCTTCTTCCGGGCCCCGCGCTCTCTCGGGCG 230

QY      181 CGAGTTTCAGGACGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 240
Db      231 CGAGTTTCAGGACGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 290

QY      241 CCGCG 245
Db      291 CCGCG 295

RESULT 3
US-09-949-016-12197
; Sequence 12197, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match      100.0%; Score 245; DB 4; Length 44960;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 60
```

```
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12197
; LENGTH: 44952
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(44952)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12197

Query Match      100.0%; Score 245; DB 4; Length 44952;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 60
Db      1811 CCCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 1870

QY      61 CCGCCTCTCCGCGCGGACCCGCCCGCTCCCGACCCCTCCCGGTCGCCGCGGCCACCCC 120
Db      1871 CCGCCTCTCCGCGCGGACCCGCCCGCTCCCGACCCCTCCCGGTCGCCGCGGCCACCCC 1930

QY      121 CTTCCGGGCCCCCAGCCGCTCCCTTCTTCCGGGCCCCGCGCTCTCTCGGGCG 180
Db      1931 CTTCCGGGCCCCCAGCCGCTCCCTTCTTCCGGGCCCCGCGCTCTCTCGGGCG 1990

QY      181 CGAGTTTCAGGACGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 240
Db      1991 CGAGTTTCAGGACGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 2050

QY      241 CCGCG 245
Db      2051 CCGCG 2055

RESULT 4
US-09-949-016-17583
; Sequence 17583, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17583
; LENGTH: 44960
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(44960)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17583

Query Match      100.0%; Score 245; DB 4; Length 44960;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCCCCCTTCCACCTTCCAGCT 60
```

Db 1811 CCCACGTCGGGAGGAGTGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGCT 1870
Qy 61 CCGCTCTCTCCGCGGAGACCCGCGCCCTCCCGGCTCCCGGCTCCCGGCGCCAGCCC 120
Db 1871 CCGCTCTCTCCGCGGAGACCCGCGCCCTCCCGGCTCCCGGCTCCCGGCGCCAGCCC 1930
Qy 121 CCTCGGCGCTCCAGACCCCTCCCTTCTCTTTCGCGGCGCCCGCCCTCTCTCTCGCGCG 180
Db 1931 CCTCGGCGCTCCAGACCCCTCCCTTCTCTTTCGCGGCGCCCGCCCTCTCTCTCGCGCG 1990
Qy 181 CGAGTTTCAGGACGCTGCTCTCTGCGCAGCTGGGAGCCCTGCGCCCGGCCACCC 240
Db 1991 CGAGTTTCAGGACGCTGCTCTCTGCGCAGCTGGGAGCCCTGCGCCCGGCCACCC 2050
Qy 241 CCGCG 245
Db 2051 CCGCG 2055

RESULT 5
US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. 6492171
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Preler
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733.294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
; LOCATION: (25394)...(25549)

; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
; NAME/KEY: exon
; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
; US-09-733-294A-30

Query Match 100.0%; Score 245; DB 4; Length 51552;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCACGTCGGGAGGAGTGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGCT 60
Db 11029 CCCACGTCGGGAGGAGTGGGACCCGGGACCCCGTCTGCCCCCTTACCTTCCAGCT 11088

```
QY 61 CCGCTCTCTCCGGCGGACCCCGCGTCCGACCCCTCCCGGCTCCCGGCGCCAGCCC 120
|||
Db 11089 CCGCTCTCTCCGGCGGACCCCGCGTCCGACCCCTCCCGGCTCCCGGCGCCAGCCC 11148

QY 121 CTTCCGGGCGCTCCAGCCCTCCCTTCTTTCGGGGCGCCGCGCTCTCTCGGGCG 180
|||
Db 11149 CTTCCGGGCGCTCCAGCCCTCCCTTCTTTCGGGGCGCCGCGCTCTCTCGGGCG 11208

QY 181 CGAGTTTCAGGACGCTGGTCTCTGTCGGCACGTGGGAAGCCCTGGCCCGGCCACCC 240
|||
Db 11209 CGAGTTTCAGGACGCTGGTCTCTGTCGGCACGTGGGAAGCCCTGGCCCGGCCACCC 11269

QY 241 CCGCG 245
|||
Db 11269 CCGCG 11273

RESULT 6
US-09-244-438-17
; Sequence 17, Application US/09244438
; Patent No. 677203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; TITLE OF INVENTION: Regulatory Sequences and Methods of Using
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-17

Query Match 99.6%; Score 244; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.6e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCACCTGGCGGAGGACTGGGACCCGGGACCCCGGACCCGTCCTGCCCCCTTCACTTCCAGCTC 61
|||
Db 52 CCACCTGGCGGAGGACTGGGACCCGGGACCCCGGACCCGTCCTGCCCCCTTCACTTCCAGCTC 111

QY 62 CGCTCTCTCCGGCGGACCCCGGCTCCGACCCCTCCCGGCTCCCGGCGCCAGCCCC 121
|||
Db 112 CGCTCTCTCCGGCGGACCCCGGCTCCGACCCCTCCCGGCTCCCGGCGCCAGCCCC 171

QY 122 CTCGGGCGCTCCAGCCCTCCCTTCTTTCGGGGCGCCGCGCTCTCTCGGGCGCG 181
|||
Db 172 CTCGGGCGCTCCAGCCCTCCCTTCTTTCGGGGCGCCGCGCTCTCTCTCGGGCGCG 231

QY 182 GAGTTTCAGGACGCTGGTCTCTGTCGGCACGTGGGAAGCCCTGGCCCGGCCACCCC 241
|||
Db 232 GAGTTTCAGGACGCTGGTCTCTGTCGGCACGTGGGAAGCCCTGGCCCGGCCACCCC 291

QY 242 CCGCG 245
|||
Db 292 CCGCG 295

RESULT 7
US-09-402-181B-6
; Sequence 6, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
```

```
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 4321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1..4321
OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
FEATURE:
NAME/KEY: intron
LOCATION: 2702..2804
OTHER INFORMATION: /note= "intron 1"
FEATURE:
NAME/KEY: intron
LOCATION: 4160..4313
OTHER INFORMATION: /note= "intron 2"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-402-181B-6
```

```
Query Match          99.6%; Score 244; DB 4; Length 4321;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 61
Db 2239 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 2298

QY 62 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 121
Db 2299 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 2358

QY 122 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 181
Db 2359 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 2418

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 241
Db 2419 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 2478

QY 242 CGCG 245
Db 2479 CGCG 2482

RESULT 8
US-09-783-203-1
; Sequence 1, Application US/09783203
; Patent No. 6576464
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gold, Joseph
; APPLICANT: Lebkowski, Jane
; TITLE OF INVENTION: Tpacked stem cells
; FILE REFERENCE: 096/003
; CURRENT APPLICATION NUMBER: US/09/783,203
; CURRENT FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,443
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/253,357
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-783-203-1

Query Match          99.6%; Score 244; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 61
Db 13301 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 13360

QY 62 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 121
Db 13361 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 13420

QY 122 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 181
Db 13421 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 13480

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 241
Db 13481 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 13540

QY 242 CGCG 245
Db 13541 CGCG 13544

RESULT 9
US-09-994-427A-1
; Sequence 1, Application US/09994427A
; Patent No. 6713055
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER
; FILE REFERENCE: 083,002
; CURRENT APPLICATION NUMBER: US/09/994,427A
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 60/253,395
; PRIOR FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-994-427A-1

Query Match          99.6%; Score 244; DB 4; Length 15418;
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 61
Db 13301 CCCAGTGGCGGAGGAGTGGGGACCCGGGACCCGGGACCCGGTCTGCCCCCTTACCTTCCAGCTC 13360

QY 62 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 121
Db 13361 CGCTCTCTCCGCGGAGGAGTGGGGACCCGGTCCGACCCCTCCCGGGTCCCGGCCACAGCCCC 13420

QY 122 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 181
Db 13421 CTCGGGGCCCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTTCGGGGGCG 13480

QY 182 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 241
Db 13481 GAGTTTCAGGACGCTGCTGCTGCGACGTGGGAAGCCCTGGGCCCGGCCACCCCC 13540

QY 242 CGCG 245
Db 13541 CGCG 13544

RESULT 10
US-09-244-438-1
; Sequence 1, Application US/09244438
; Patent No. 6777203
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/09/244,438
; CURRENT FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15418
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-09-244-438-1

Query Match          99.6%; Score 244; DB 4; Length 15418;
```

```
Best Local Similarity 100.0%; Pred. No. 4.4e-41;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCTC 61
Db 13301 CCCAGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCTC 13360
QY 62 CGCTCTCTCCGGCGGAGACCCCGCCCGCTGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 121
Db 13361 CGCTCTCTCCGGCGGAGACCCCGCCCGCTGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 13420
QY 122 CTCGGGCGCTCCAGCCCTCCCTTCTCTTCCGGGGCCCGGCTCTCTCTCGGGGGC 181
Db 13421 CTCGGGCGCTCCAGCCCTCCCTTCTCTTCCGGGGCCCGGCTCTCTCTCGGGGGC 13480
QY 182 GAGTTTCAGGACGCTGGCTCTGCTGGCACGTGGGAAGCCCTGGCCCCCGCCACCCC 241
Db 13481 GAGTTTCAGGACGCTGGCTCTGCTGGCACGTGGGAAGCCCTGGCCCCCGCCACCCC 13540
QY 242 CGCG 245
Db 13541 CGCG 13544

RESULT 11
US-09-916-510A-8
; Sequence 8, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9908815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-916-510A-8

Query Match 93.8%; Score 229.8; DB 4; Length 314;
Best Local Similarity 98.8%; Pred. No. 3.4e-38;
Matches 242; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCT 60
Db 71 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCT 130
QY 61 CGCTCTCTCCGGCGGAGCCCGCCCGCTGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 131 CGCTCTCTCCGGCGGAGCCCGCCCGCTGCTCCGACCCCTCCCGGGTCCCGGGCCAGCCC 190
QY 121 CTCTCCGGGCTCCAGCCCTCCCTCTCTCTTCCGGGCGCCCGCCCTCTCTCTCGGGCG 180
Db 191 CTCTCCGGG-CTTCCAGCCCCCCCCCTTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 249
QY 181 CGAGTTTTCAGGACGCTGGCTCTGCTGGCGACGTGGGAAGCCCTGGCCCCCGCCACCCC 240
Db 250 CGAGTTTTCAGGACGCTGGCTCTGCTGGCGACGTGGGAAGCCCTGGCCCCCGCCACCCC 309
QY 241 CGCG 245
Db 310 CGCG 314

RESULT 12
US-08-912-951-6
; Sequence 6, Application US/08912951
; Patent No. 6475789
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; TITLE OF INVENTION: THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,951
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-912-951-6

Query Match 83.4%; Score 204.4; DB 4; Length 4200;
Best Local Similarity 94.7%; Pred. No. 4.5e-33;
Matches 233; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 2 CCCACGTGGCGAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCTC 61
Db 2067 CCCACGTGGCGAAGGAGCTGGGGACCCGGGACCCGCTCTGCGCCCTTACCTTCCAGCTC 2126
QY 62 CGCTCTCTCCGGCGGAGACCCCGCCCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGCCCC 121
```

```
Db 2127 CGCTTTCCGGGAGACCGGCGCCGCTCCGGAACCTTCCAGGTCCCGGCCAGCCCC 2186
Qy 122 CTCGGGCGCTCCAGACCCCTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCC-TCGGGCG 179
Db 2187 TTCGGGGCGCTCCAGACCCCTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCC-TCGGGCG 2246
Qy 180 GCGAGTTTCAGGACGCTGCGTCTCTGTCGCGACGTCGGGAAGCCCTGGCCCGGCCACC 239
Db 2247 GCGAGTTTCAGGACGCTGCGTCTCTGTCGCGACGTCGGGAAGCCCTGGCCCGGCCACC 2306
Qy 240 CCCGGG 245
Db 2307 CCCGGG 2312

RESULT 13
US-09-956-335-2/c
; Sequence 2, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konsantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 35871
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-2

Query Match 82.1%; Score 201.2; DB 4; Length 35871;
Best Local Similarity 98.5%; Pred. No. 2e-32;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCAGTGGCGGAGGACTGGGGACCCGGGACCCCGTCCCGGCTTCCCTTCCAGTTC 61
Db 34232 CCCAGTGGCGGAGGACTGGGGACCCGGGACCCCGTCCCGGCTTCCCTTCCAGTTC 34173
Qy 62 GCGCTTCTCCGGCGGAGACCCCGGCGCCGCTCCCGACCCCTCCCGGGTCCCGGCCAGCCCC 121
Db 34172 GCGCTTCTCCGGCGGAGACCCCGGCGCCGCTCCCGACCCCTCCCGGGTCCCGGCCAGCCCC 34113
Qy 122 CTCGGGCGCTCCAGACCCCTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCTCTCGGGCGCG 181
Db 34112 CTCGGGCGCTCCAGACCCCTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCTCTCGGGCGCG 34053
Qy 182 GAGTTTCAGGACGCTGCGTCTCG 207
Db 34052 GAGTTTCAGGACGCTGATTACTGC 34027

RESULT 14
US-09-956-335-1/c
; Sequence 1, Application US/09956335
; Patent No. 6627190
; GENERAL INFORMATION:
; APPLICANT: WOLD, William
; APPLICANT: TOTH, Karoly
; APPLICANT: KUPPASWAMI, Mohan
; APPLICANT: DORONIN, Konsantin
; TITLE OF INVENTION: RECOMBINANT ADENOVIRUS VECTORS THAT ARE
; TITLE OF INVENTION: REPLICATION-COMPETENT IN TERT-EXPRESSING CELLS
; FILE REFERENCE: 16153-8394
; CURRENT APPLICATION NUMBER: US/09/956,335
; CURRENT FILING DATE: 2001-09-19
```

```
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 35978
; TYPE: DNA
; ORGANISM: Adenovirus
US-09-956-335-1

Query Match 82.1%; Score 201.2; DB 4; Length 35978;
Best Local Similarity 98.5%; Pred. No. 2e-32;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCAGTGGCGGAGGACTGGGGACCCGGGACCCCGTCCCGGCTTCCCTTCCAGTTC 61
Db 34339 CCCAGTGGCGGAGGACTGGGGACCCGGGACCCCGTCCCGGCTTCCCTTCCAGTTC 34280
Qy 62 GCGCTTCTCCGGCGGAGACCCCGGCGCCGCTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 121
Db 34279 GCGCTTCTCCGGCGGAGACCCCGGCGCCGCTTCCCGACCCCTTCCCGGGTCCCGGCCAGCCCC 34220
Qy 122 CTCGGGCGCTCCAGACCCCTTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCTCTCGGGCGCG 181
Db 34219 CTCGGGCGCTCCAGACCCCTTCCCTTCC-TTTCGGGGCGCCCGCCCTCTCTCTCGGGCGCG 34160
Qy 182 GAGTTTCAGGACGCTGCGTCTCG 207
Db 34159 GAGTTTCAGGACGCTGATTACTGC 34134

RESULT 15
US-08-974-549A-6
; Sequence 6, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
```

```
/ FILING DATE: 09-MAY-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-OCT-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-OCT-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4335 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..4335
/ OTHER INFORMATION: /note= "genomic DNA insert of pGRN144"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 2715..2818
/ OTHER INFORMATION: /note= "intron 1"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 4173..4326
/ OTHER INFORMATION: /note= "intron 2"
/
/ US-08-974-549A-6

Query Match      81.6%; Score 199.8; DB 3; Length 4335;
Best Local Similarity 96.0%; Pred. No. 3.9e-32;
Matches 237; Conservative 0; Mismatches 7; Indels 3; Gaps 3;

QY      2  CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCCCCCTTCACCTTCAGCTC 61
Db      2249  CCCACGTGGCGGAGGACTGGGGACCCGGGACCCGGTCTCTGCCCCCTTCACCTTCAGCTC 2308

QY      62  CGCCTCCTCCGCGCGG-ACCCGCGCCGTCCTCC-ACCCCTCCGGGTCCCGGCCAGCC 119
Db      2309  CGCCTCGTCCGCGCGGAAACCCGCGCCGTCCTCCGGAACCTTCCTGGGTCCCGGCCAGCC 2368

QY      120  CCCTCCGGGCGCTCCAGCCCTCTCCCTTCC-TTTCGGGCGCCCGCCCTCTCTCGCGG 178
Db      2369  CCTTCGGGGCCATCCAGCCCGTCCCGTTCTTTTCGGGCGCCCGCCCTCTCTCGCGG 2428

QY      179  CGCGAGTTTCAGGACGCTGGGTCTGTGTGCGACGTGGGAAGCCCTGGCCCCCGGCCAC 238
Db      2429  CGCGAGTTTCAGGACGCTGGGTCTGTGTGCGACGTGGGAAGCCCTGGCCCCCGGCCAC 2488

QY      239  CCCCCG 245
Db      2489  CCCCCG 2495
```

Search completed: April 9, 2005, 07:05:40
Job time : 78.8505 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 05:34:49 ; Search time 1229.58 Seconds
(without alignments)
9654.950 Million cell updates/sec

Title: US-10-081-969-94
Perfect score: 245
Sequence: 1 cccacgtggcggaggact.....tggcccgccacccccgcg 245

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245	100.0	245	6	AX817858 Sequence
2	245	100.0	261	6	AR455896 Sequence
3	245	100.0	955	6	AX817781 Sequence
4	245	100.0	5126	6	AX003120 Sequence
5	245	100.0	5491	9	AB016767 Homo sapi
6	245	100.0	5928	6	AR455897 Sequence
7	245	100.0	11276	6	AX003122 Sequence
8	245	100.0	26414	9	HS1871 Homo sapi
9	245	100.0	51552	6	AR266023 Sequence
10	244	99.6	397	6	AX817857 Sequence
11	244	99.6	2043	9	AF098956 Homo sapi
12	244	99.6	4321	6	AR390473 Sequence
13	244	99.6	4356	9	AF097365 Homo sapi
14	244	99.6	15332	9	AF121948 Homo sapi
15	244	99.6	15418	6	AR342806 Sequence
16	244	99.6	15418	6	AR490112 Sequence
17	244	99.6	15418	6	AX453025 Sequence
18	244	99.6	15418	6	AX498409 Sequence
19	244	99.6	15418	6	AX504952 Sequence

20	244	99.6	92564	9	AY007685 Homo sapi
c 21	244	99.6	161252	2	AC114955 Homo sapi
c 22	244	99.6	202305	9	AC114291 Homo sapi
c 23	233	95.1	170646	2	AC123545 Pan trogl
24	229.8	93.8	314	6	BD262062 Antineopl
25	229.8	93.8	314	6	AR303036 Sequence
26	229.8	93.8	314	6	AX036796 Sequence
27	229.8	93.8	12213	9	AF114847 Homo sapi
28	229	93.5	2132	9	AF325900 Homo sapi
29	205	83.7	1404	9	AB018788 Homo sapi
30	204.4	83.4	4200	6	AR243331 Sequence
c 31	201.2	82.1	35871	6	AR403724 Sequence
c 32	201.2	82.1	35978	6	AR403723 Sequence
c 33	200.8	82.0	403	6	AX817785 Sequence
34	199.8	81.6	4335	6	E36796
35	199.8	81.6	4335	6	AR393087 Sequence
36	199.8	81.6	4335	6	AX810041 Sequence
37	199.8	81.6	4335	6	BD011047 Human tel
c 38	198	80.8	1677	6	AR403725 Sequence
c 39	186	75.9	170946	2	AC117933 Papio anu
c 40	186	75.9	183506	2	AC122155 Papio anu
c 41	183.2	74.8	4356	6	AX356510 Sequence
c 42	158.6	64.7	1404	6	AX280012 Sequence
43	93.6	38.2	124	6	AR393446 Sequence
44	89	36.3	4356	6	AX356509 Sequence
45	77	31.4	78	6	AR455879 Sequence

ALIGNMENTS

RESULT 1
AX817858
LOCUS AX817858 245 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 94 from Patent WO02067861.
ACCESSION AX817858
VERSION AX817858.1 GI:39723053
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Oncolytic adenoviral vectors
TITLE Patent: WO 02067861-A 94 06-SEP-2002;
JOURNAL Location/Qualifiers
FEATURES
source 1..245
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
promoter 1..245
/note="A 245 bp fragment of the hTERT promoter"

QY	1	CCCCACGTGGCGGAGGACTGGGACCCCGGACCCCGCTCCCGGTCCTCCCTTCCAGTTCAGCT 60
Db	1	CCCCACGTGGCGGAGGACTGGGACCCCGGACCCCGCTCCCGGTCCTCCCTTCCAGTTCAGCT 60
QY	61	CCGCTCTCTCCGCGGACCCCGGACCCCGCTCCCGGTCCTCCCGGTCCTCCCGGTCCTCCCGG 120
Db	61	CCGCTCTCTCCGCGGACCCCGGACCCCGCTCCCGGTCCTCCCGGTCCTCCCGGTCCTCCCGG 120
QY	121	CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGCGGCCCCCGCCCTCTCTCTCGCGGCG 180
Db	121	CCTCGGGCCCTCCAGCCCTCCCTTCTTTCGCGGCCCCCGCCCTCTCTCTCGCGGCG 180
QY	191	CGAGTTTCAGGAGCGCTGCTCTGTGCGGACGTGGGAAGCCCTGGCCCGCCGCGCACCC 240

```

Db      181 CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 240
Qy      241 CCGCG 245
Db      241 CCGCG 245

RESULT 2
AR455896
LOCUS      261 bp      DNA      linear      PAT 20-FEB-2004
DEFINITION Sequence 24 from patent US 6686159.
ACCESSION AR455896
VERSION    AR455896.1 GI:42690788
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 261)
AUTHORS     Andrews,W.H., Foster,C.A., Frazer,S. and Mohammadpour,H.
TITLE        Methods and compositions for modulating telomerase reverse
transcriptase (TERT) expression
JOURNAL     Patent: US 6686159-A 24 03-FEB-2004;
FEATURES     Location/Qualifiers
             1..261
             /organism="unknown"
             /mol_type="genomic DNA"

ORIGIN

Query Match      100.0%; Score 245; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 4.7e-29;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1   CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 60
Db      14   CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 73

Qy      61   CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 120
Db      74   CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 133

Qy      121  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 180
Db      134  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 193

Qy      181  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 240
Db      194  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 253

Qy      241  CCGCG 245
Db      254  CCGCG 258

RESULT 3
AX817781/c
LOCUS      955 bp      DNA      linear      PAT 10-DEC-2003
DEFINITION Sequence 17 from Patent WO2067861.
ACCESSION AX817781
VERSION    AX817781.1 GI:39722976
KEYWORDS   synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Oncolytic adenoviral vectors
TITLE        Patent: WO 02067861-A 17 06-SEP-2002;
JOURNAL     Location/Qualifiers
FEATURES     1..955
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Viral vector sequence"

```

```

misc_feature 1..955
/note="Fig.47. Sequence of the right end of
Ar17pAE2fFrtex"

ORIGIN

Query Match      100.0%; Score 245; DB 6; Length 955;
Best Local Similarity 100.0%; Pred. No. 2.9e-29;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1   CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 60
Db      500   CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 441

Qy      61   CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 120
Db      440   CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 381

Qy      121  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 180
Db      380  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 321

Qy      181  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 240
Db      320  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 261

Qy      241  CCGCG 245
Db      260  CCGCG 256

RESULT 4
AX003120
LOCUS      5126 bp      DNA      linear      PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9933998
ACCESSION AX003120
VERSION    AX003120.1 GI:9926982
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Wick,M. and Hagen,G.
TITLE        Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL     Patent: WO 9933998-A 1 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)
FEATURES     Location/Qualifiers
             1..5126
             /organism="Homo sapiens"
             /mol_type="unassigned DNA"
             /db_xref="taxon:9606"

ORIGIN

Query Match      100.0%; Score 245; DB 6; Length 5126;
Best Local Similarity 100.0%; Pred. No. 1.6e-29;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1   CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 60
Db      4879  CCCACGTGGCGGAGGACTGGGGACCCGGGACCCCGTCTCTGCGCCCTTCACTTCCAGCT 4938

Qy      61   CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 120
Db      4939  CCGCTCTCTCCGCGCGGACCCCGCCCGTCCGACCCCTCCCGGGTCCCGGCCACAGCCC 4998

Qy      121  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 180
Db      4999  CTTCCGGGCTCCAGCCCTCCCTTCTTCCGGGCGCCCGCCCTCTCTCGGGCG 5058

Qy      181  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 240
Db      5059  CGAGTTTCAGGACGCTGCTGCTGCTGCGACGTTGGGAAGCCCTGGGCCCGGCCACCC 5118

```

```

QY      241  CCGCG 245
Db      5119  CCGCG 5123

RESULT 5
AB016767
LOCUS   Homo sapiens gene for telomerase transcriptase, partial cds.
DEFINITION
ACCESSION AB016767
VERSION   AB016767.1 GI:4239069
KEYWORDS telomerase transcriptase; hTERT.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Takakura,M., Kyo,S., Kanaya,T., Hirano,H., Takeda,J., Yutsudo,M.
          and Inoue,M.
TITLE    Cloning of human telomerase catalytic subunit (hTERT) gene promoter
          and identification of proximal core promoter sequences essential
          for transcriptional activation in immortalized and cancer cells
          Cancer Res. 59 (3), 551-557 (1999)
JOURNAL  59137484
MEDLINE  9973199
REFERENCE
AUTHORS Takakura,M., Kyo,S., Kanaya,T., Takeda,J. and Inoue,M.
TITLE    Direct Submision
JOURNAL  Submitted (04-AUG-1998) Masahiro Takakura, Kanazawa University,
          School of Medicine, Department of Obstetrics and Gynecology; 13-1,
          Takaranachi, Kanazawa, Ishikawa 920-0934, Japan
          (E-mail: takakura@med.kanazawa-u.ac.jp. Tel:81-76-265-2425,
          Fax:81-76-234-4266)
FEATURES             Location/Qualifiers
     source           1..5491
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     GC_signal        3250..3255
                     /note="telomerase transcriptase promoter"
     GC_signal        3331..3336
                     /note="telomerase transcriptase promoter"
     gene             3338..5491
                     /gene="hTERT"
     exon             3338..3633
                     /gene="hTERT"
                     /number=1
     5'UTR            3338..3414
                     /gene="hTERT"
                     /evidence=experimental
     CDS              join(3415..3633,3738..5088)
                     /product="telomerase transcriptase"
                     /protein_id="BAA74724.1"
                     /db_xref="GI:4239870"
                     /translation="MPRAPRCRAVRLSHRYEVLPLATFVRRLGPOGWRLVORGDP
                     RAFLVAQCLVCPWDAPPPAAPSFRQVSLKELVARVLQRLCERAKVLAFGFA
                     LLDGARGPPPEAFTTSVRSYLPNTVDALRGSGWGLLRLRVGGDVLVHLLARCMALFV
                     LVAPSCAYCGPFLYQIGAAQTQAPPPPHASGPRRLGCRANWHSVREAGVPLGLPA
                     PGARRGSASLSLPKPRRGAAPPEPTPVQGSWAHPGRTGRPSDRGFCVVSIPA
                     RPAEATSLGALSGTRISHPSVQHQHAGPSTSRPPRPMDTPCPVVAETKHFVLS
                     SGDKQLRPSFLLSLRPLITGABRLVETIFLGSPPGCGQLPAGCAPCPATKCGPC
                     FNSCLGTRSPATGSSRRARCELRSPOQPVSVGRSPRALRRPRRTOTPVWACS
                     CSASTAPLAGVRLAGLAPAGAPRLGLQAQRRRLRNTKFIISLGHAKLSLQELT
                     WKMSVRDCAWLRSP"
                     3634..3737
                     /gene="hTERT"
                     /number=1
     intron            3738..5088
                     /gene="hTERT"
                     /number=2

QY      241  CCGCG 245
Db      5119  CCGCG 5123

Query Match      100.0%; Score 245; DB 9; Length 5491;
Best Local Similarity 100.0%; Pred. No. 1.6e-29; Indels 0; Gaps 0;
Matches 245; Conservative 0; Mismatches 0;

QY      1  CCCACAGTGGCGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 60
Db      3170  CCCACAGTGGCGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 3229
QY      61  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCCGGGTCCCGGCCAGGCC 120
Db      3230  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCCGGGTCCCGGCCAGGCC 3289
QY      121  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db      3290  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 3349
QY      181  CGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAAAGCCCTGGCCCGGCACCC 240
Db      3350  CGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAAAGCCCTGGCCCGGCACCC 3409
QY      241  CCGCG 245
Db      3410  CCGCG 3414

RESULT 6
AR455897
LOCUS   Sequence 25 from patent US 6686159.
DEFINITION
ACCESSION AR455897
VERSION   AR455897.1 GI:42690789
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5928)
AUTHORS Andrews,W.H., Foster,C.A., Fraser,S. and Mohammadpour,H.
TITLE    Methods and compositions for modulating telomerase reverse
          transcriptase (TERT) expression
JOURNAL  Patent: US 6686159-A 25 03-FEB-2004;
FEATURES             Location/Qualifiers
     source           1..5928
                     /organism="unknown"
                     /mol_type="genomic DNA"

QY      1  CCCACAGTGGCGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 60
Db      51  CCCACAGTGGCGAGGAGTGGGACCCGGGACCCGGGACCCGCTCTGCCCCCTTTCACCTTCCAGCT 110
QY      61  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCGGGTCCCGGCCAGGCC 120
Db      111  CCGCTCTCTCCGCGGAGACCCCGCCCGCTTCCGACCCCTCCGGGTCCCGGCCAGGCC 170
QY      121  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db      171  CCTCGGGCCCTCCAGCCCTCCCTTCTTCCGGGGCCCGCCCTCTCTCTCGGGCG 230
QY      181  CGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAAAGCCCTGGCCCGGCACCC 240
Db      231  CGAGTTTCAGGACGCTGCGTCTGCTGCGACAGTGGAAAGCCCTGGCCCGGCACCC 290
QY      241  CCGCG 245
Db      5119  CCGCG 5123

```

Db 291 CCGCG 295

RESULT 7
AX003122 11276 bp DNA linear PAT 24-AUG-2000
LOCUS Sequence 3 from Patent WO9933998.
DEFINITION AX003122
ACCESSION AX003122
VERSION AX003122.1 GI:9926984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Wick, M., and Hagen, G.
TITLE Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof
JOURNAL WICK MARESA (DE); BAYER AG (DE)
PATENT: WO 9933998-A 3 08-JUL-1999;
FEATURES
Location/Qualifiers
1. .11276
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 245; DB 6; Length 11276;
Best Local Similarity 100.0%; Pred. No. 1.2e-29;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGCGGAGGACTGGGGACCCGGGACCCGGTCTGCGCCCTTCCAGCT 60
Db 11029 CCCACGTGCGGAGGACTGGGGACCCGGGACCCGGTCTGCGCCCTTCCAGCT 11088
Qy 61 CCGCTCTCTCGCGGGACCCCGCCGCTCCGAGACCCCTCCGGGTCCCGGCCAGCC 120
Db 11089 CCGCTCTCTCGCGGGACCCCGCCGCTCCGAGACCCCTCCGGGTCCCGGCCAGCC 11148
Qy 121 CTTCCGGGCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGGGGG 180
Db 11149 CTTCCGGGCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGGGGG 11208
Qy 181 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCC 240
Db 11209 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCC 11268
Qy 241 CCGCG 245
Db 11269 CCGCG 11273

RESULT 8
HSTERT1 26414 bp DNA linear PRI 13-MAY-1999
LOCUS Homo sapiens telomerase reverse transcriptase (TERT) gene, exons
DEFINITION 1-6.
ACCESSION AF128893
VERSION AF128893.1 GI:4808970
KEYWORDS
SEGMENT 1 of 2
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 26414)
AUTHORS Wick, M., Zubov, D. and Hagen, G.
TITLE Genomic organization and promoter characterization of the gene
encoding the human telomerase reverse transcriptase (hTERT)
JOURNAL Gene 232 (1), 97-106 (1999)
MEDLINE 99267414
PUBMED 10333526
REFERENCE 2 (bases 1 to 26414)

Wick, M., Zubov, D. and Hagen, G.
Direct Submission
Submitted (16-FEB-1999) Dept. of Mol. Biol., Bayer AG Leverkusen,
ZF-BTM, Bldg. Q18, Leverkusen D-51368, Germany

FEATURES
source
1. .26414
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
promoter
1. .>11211
/gene="TERT"
exon
11212. .11492
/gene="TERT"
/number=1
5' UTR
11212. .11273
/gene="TERT"
exon
11597. .12950
/gene="TERT"
/number=2
exon
21567. .21762
/gene="TERT"
/number=3
exon
23852. .24032
/gene="TERT"
/number=4
exon
24720. .24899
/gene="TERT"
/number=5
exon
25394. .25549
/gene="TERT"
/number=6

ORIGIN
Query Match 100.0%; Score 245; DB 9; Length 26414;
Best Local Similarity 100.0%; Pred. No. 8.8e-30;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGCGGAGGAGCTGGGGACCCGGGACCCGGTCTGCGCCCTTCCAGCT 60
Db 11029 CCCACGTGCGGAGGAGCTGGGGACCCGGTCTGCGCCCTTCCAGCT 11088
Qy 61 CCGCTCTCTCGCGGGACCCCGCCGCTCCGAGACCCCTCCGGGTCCCGGCCAGCC 120
Db 11089 CCGCTCTCTCGCGGGACCCCGCCGCTCCGAGACCCCTCCGGGTCCCGGCCAGCC 11148
Qy 121 CTTCCGGGCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGGGGG 180
Db 11149 CTTCCGGGCTCCAGCCCTCCCTCTCTTTCGGGGCCCGCCCTCTCTCGGGGG 11208
Qy 181 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCC 240
Db 11209 CGAGTTTCAGGACGCGTGGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGCCACCC 11268
Qy 241 CCGCG 245
Db 11269 CCGCG 11273

RESULT 9
AR266023 51552 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 30 from patent US 6492171.
DEFINITION AR266023
ACCESSION AR266023
VERSION AR266023.1 GI:29694869
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51552)
AUTHORS Monia, B.P., Gaarde, W.A., Freier, S.M. and Wancewicz, E.
TITLE Antisense modulation of TERT expression
JOURNAL Patent: US 6492171-A 30 10-DEC-2002;
FEATURES Location/Qualifiers


```
QY 182 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 241
|||||
Db 1657 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 1716

QY 242 CGCG 245
|||||
Db 1717 CGCG 1720

RESULT 12
AR390473
LOCUS AR390473 4321 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 6 from patent US 6610839.
ACCESSION AR390473
VERSION AR390473.1 GI:40112397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 4321)
MORIN,G.B. and ANDREWS,W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 6 26-AUG-2003;
FEATURES
source Location/Qualifiers
1. .4321
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 99.6%; Score 244; DB 6; Length 4321;
Best Local Similarity 100.0%; Pred. No. 2.4e-29;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCACAGTGGCGAGGACTGGGACCCGGGACCCGTCCTCTGCCCCCTTACCTTCCAGCTC 61
|||||
Db 2239 CCACAGTGGCGAGGACTGGGACCCGGGACCCGTCCTCTGCCCCCTTACCTTCCAGCTC 2298

QY 62 CGCTCTCTCGCGGACCCGCGCCGTCGCGACCCCTCCCGGTCCTCCGGGCCAGCCCC 121
|||||
Db 2299 CGCTCTCTCGCGGACCCGCGCCGTCGCGACCCCTCCCGGTCCTCCGGGCCAGCCCC 2358

QY 122 CTCGGGGCTCCAGCCCTCCCTTCTTCCGGGGCCGCGCCCTCTCTCGGGGCGC 181
|||||
Db 2359 CTCGGGGCTCCAGCCCTCCCTTCTTCCGGGGCCGCGCCCTCTCTCGGGGCGC 2418

QY 182 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 241
|||||
Db 2419 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 2478

QY 242 CGCG 245
|||||
Db 2479 CGCG 2482

RESULT 13
AF097365
LOCUS AF097365 4356 bp DNA linear PRI 02-FEB-1999
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, promoter
and partial cds.
ACCESSION AF097365
VERSION AF097365.1 GI:4210970
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4356)
CONG,Y.S., WEN,J. and BACCHETTI,S.
TITLE The human telomerase catalytic subunit hTERT: organization of the
gene and characterization of the promoter
JOURNAL Hum. Mol. Genet. 8 (1), 137-142 (1999)
MEDLINE 99105927
PUBMED 9887342
```

```
REFERENCE 2 (bases 1 to 4356)
AUTHORS Cong,Y.S., Wen,J. and Bacchetti,S.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) Pathology, McMaster University, 1200 Main
St. W., Hamilton, ON L8N 3Z5, Canada
FEATURES
source Location/Qualifiers
1. .4356
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
1. .>4356
/gene="TERT"
1. .3996
/gene="TERT"
Join(<3997..4215,4320..>4356)
/gene="TERT"
/product="telomerase reverse transcriptase"
Join(3997..4215,4320..>4356)
/gene="TERT"
/codon_start=1
/product="telomerase reverse transcriptase"
/protein_id="AAD12057.1"
/db_xref="GI:4210971"
/translation="MPRAPRCRAVPSLLRSHYREVLPLATFVRRILGPGQWRLVQRGDP
AAFRALVAQCLVCPWDARPPPAAPSPRQVSCLELVARVL"

ORIGIN
Query Match 99.6%; Score 244; DB 9; Length 4356;
Best Local Similarity 100.0%; Pred. No. 2.4e-29;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCACGTGGCGAGGACTGGGACCCGGGACCCGTCCTCTGCCCCCTTACCTTCCAGCTC 61
|||||
Db 3753 CCCACGTGGCGAGGACTGGGACCCGGGACCCGTCCTCTGCCCCCTTACCTTCCAGCTC 3812

QY 62 CGCTCTCTCGCGGACCCGCGCCGTCGCGACCCCTCCCGGTCCTCCGGGCCAGCCCC 121
|||||
Db 3813 CGCTCTCTCGCGGACCCGCGCCGTCGCGACCCCTCCCGGTCCTCCGGGCCAGCCCC 3872

QY 122 CTCGGGGCTCCAGCCCTCCCTTCTTCCGGGGCCGCGCCCTCTCTCGGGGCGC 181
|||||
Db 3873 CTCGGGGCTCCAGCCCTCCCTTCTTCCGGGGCCGCGCCCTCTCTCGGGGCGC 3932

QY 182 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 241
|||||
Db 3933 GAGTTTCAGCAGCGTGGTCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCC 3992

QY 242 CGCG 245
|||||
Db 3993 CGCG 3996

RESULT 14
AF121948
LOCUS AF121948 15332 bp DNA linear PRI 11-APR-1999
DEFINITION Homo sapiens telomerase reverse transcriptase (TERT) gene, partial
cds.
ACCESSION AF121948
VERSION AF121948.1 GI:4580662
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 15332)
GREENBERG,R.A., O'HAGAN,R.C., DENG,H., XIAO,Q., HANN,S.R.,
ADAMS,R.R., LICHTSTEINER,S., CHIN,L., MORIN,G.B. and DEPINHO,R.A.
TITLE Telomerase reverse transcriptase gene is a direct target of c-Myc
but is not functionally equivalent in cellular transformation
JOURNAL Oncogene 18 (5), 1219-1226 (1999)
MEDLINE 99144726
PUBMED 10022128
```

REFERENCE 2 (bases 1 to 15332)
AUTHORS Morin,G.B., Carlos,R. and Adams,R.R.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-1999) Geron Corporation, 230 Constitution Drive,
Menlo Park, CA 94025, USA
FEATURES
source Location/Qualifiers
1..15332
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1..>15332
/gene="TERT"
1..13446
/gene="TERT"
Join(13447..13720,13825..>15178)
/gene="TERT"
/product="telomerase reverse transcriptase"
Join(13502..13720,13825..>15178)
/gene="TERT"
/codon_start=1
/product="telomerase reverse transcriptase"
/protein_id="AAD24464.1"
/db_xref="GI:4580663"
/translation="MPRAPRCRAVRLSHRVPLATFVRLGPGWELVORGP
AAPRALVAQVLPWDARPPAAPSPFQVNSCLKELVARVLQRCERAKNVLAFGFA
LLDARGGPPPAFTSVRSYLPTNTDALRGSGAWGLLLRRVDDVLVHLLARALFV
LVAPSCYQVCGPLYQIAGAATQARPPPHASGRRRLRGCRANHSVREAGVPLGLPA
PGARRRGASRSPLPKRRRGAAPERTPVQGSWAHPGRTGRSPDRGFCVVSFA
RPAEATSLGALSGTRHSPVGRHAGPPSTSRPPMDTPCPVPVAAETKHFVLS
SGDEQLRPSFLSLRSLTGABRLVETIPLSRPMPGTPRLPLPORYWQMRPL
FLELLGNHAQCPYGVLLTHCPRAVTPPAACVCAKEPKQGSVAAPBEEDTPRLVQ
LLRQHSPPQVYGFVRACLRRLVPPGLWGRHNRERFLRNTKFKISLGHAKLSLQEL
TWKMSVRDCAWLRRSP"
ORIGIN
Query Match 99.6%; Score 244; DB 9; Length 15332;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTGCGGCTTCCAGCTC 61
Db 13258 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTGCGGCTTCCAGCTC 13317
QY 62 CGCTCTCCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGCTCCCGGCCAGCCCC 121
Db 13318 CGCTCTCCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGCTCCCGGCCAGCCCC 13377
QY 122 CTCGGGGCTCCGAGCGCTCCCTTCCGCGGCGCGGCTCTCTCTCGGGGCGC 181
Db 13378 CTCGGGGCTCCGAGCGCTCCCTTCCGCGGCGCGGCTCTCTCTCGGGGCGC 13437
QY 182 GAGTTTCAGGACGCTGCTCTGCGACGCTGGGAAGCCCTGGCGCCGACCCCC 241
Db 13438 GAGTTTCAGGACGCTGCTCTGCGACGCTGGGAAGCCCTGGCGCCGACCCCC 13497
QY 242 CGCG 245
Db 13498 CGCG 13501
Search completed: April 9, 2005, 07:02:07
Job time : 1230.58 secs

JOURNAL Patent: US 6576464-A 1 10-JUN-2003;
FEATURES
source Location/Qualifiers
1..15418
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 99.6%; Score 244; DB 6; Length 15418;
Best Local Similarity 100.0%; Pred. No. 1.5e-29;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTGCGGCTTCCAGCTC 61
Db 13301 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTGCGGCTTCCAGCTC 13360
QY 62 CGCTCTCCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGCTCCCGGCCAGCCCC 121
Db 13361 CGCTCTCCGCGGAGACCCCGCCCGTCCGACCCCTCCCGGCTCCCGGCCAGCCCC 13420
QY 122 CTCGGGGCTCCGAGCGCTCCCTTCCGCGGCGCGGCTCTCTCTCGGGGCGC 181
Db 13421 CTCGGGGCTCCGAGCGCTCCCTTCCGCGGCGCGGCTCTCTCTCGGGGCGC 13480
QY 182 GAGTTTCAGGACGCTGCTCTGCGACGCTGGGAAGCCCTGGCGCCGACCCCC 241
Db 13481 GAGTTTCAGGACGCTGCTCTGCGACGCTGGGAAGCCCTGGCGCCGACCCCC 13540
QY 242 CGCG 245
Db 13541 CGCG 13544
Search completed: April 9, 2005, 07:02:07
Job time : 1230.58 secs

RESULT 15
AR342806
LOCUS AR342806 15418 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6576464.
ACCESSION AR342806
VERSION AR342806.1 GI:33738009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15418)
AUTHORS Gold,J.D. and Lebkowski,J.S.
TITLE Methods for providing differentiated stem cells

THIS PAGE BLANK (USPTO)

SECRET

TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(245)
OTHER INFORMATION: A 245 bp fragment of the hTERT promoter
US-10-081-969-94

Query Match 100.0%; Score 245; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 7.2e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 60
DB 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 60

QY 61 CGCCTCTCCGCGCGGAGACCCCGCCCGCTCCGCGACCCCTCCGCGGCTCCGCGGCGCCAGCCC 120
DB 61 CGCCTCTCCGCGCGGAGACCCCGCCCGCTCCGCGACCCCTCCGCGGCTCCGCGGCGCCAGCCC 120

QY 121 CTTCCGGGCGCTCCGCGGAGACCCCGCTCCGCTCTTTCGCGGCGCCGCTCTCTCCGCGGCG 180
DB 121 CTTCCGGGCGCTCCGCGGAGACCCCGCTCCGCTCTTTCGCGGCGCCGCTCTCTCTCCGCGGCG 180

QY 181 CGAGTTTCAGGCGAGCGCTGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 240
DB 181 CGAGTTTCAGGCGAGCGCTGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 240

QY 241 CCGCG 245
DB 241 CCGCG 245

RESULT 2

US-09-932-581-24
Sequence 24, Application US/09932581
Publication No. US20030050264A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/09/932,581
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
TYPE: DNA
ORGANISM: human
US-09-932-581-24

Query Match 100.0%; Score 245; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 60
DB 14 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 73

QY 61 CGCCTCTCCGCGCGGAGACCCCGCTCCGCTCCGCGGCTCCGCGGCGCCAGCCC 120
DB 74 CGCCTCTCCGCGCGGAGACCCCGCTCCGCTCCGCGGCTCCGCGGCGCCAGCCC 133

QY 121 CTTCCGGGCGCTCCGCGGAGACCCCGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 180
DB 134 CTTCCGGGCGCTCCGCGGAGACCCCGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 193

QY 181 CGAGTTTCAGGCGAGCGCTGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 240
DB 194 CGAGTTTCAGGCGAGCGCTGCTCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 253

QY 241 CCGCG 245
DB 254 CCGCG 258

RESULT 3

US-10-338-294-24
Sequence 24, Application US/10338294
Publication No. US20030171326A1
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Foster, Christopher A.
APPLICANT: Fraser, Stephanie
APPLICANT: Mohammadpour, Hamid
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER-005
CURRENT APPLICATION NUMBER: US/10/338,294
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US/09/932,581
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/227,865
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/230,174
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/238,345
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 261
TYPE: DNA
ORGANISM: human
US-10-338-294-24

Query Match 100.0%; Score 245; DB 16; Length 261;
Best Local Similarity 100.0%; Pred. No. 7.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 60
DB 14 CCCCAGTGGCGGAGGACTGGGGACCCGGGACCCGCTCTGCTCCGCGGCGCCGCTTCCAGCT 73

QY 61 CGCCTCTCTCCGCGCGGAGACCCCGCTCCGCGACCCCTCCCGGGTCCCGGCCAGCCC 120
DB 74 CGCCTCTCTCCGCGCGGAGACCCCGCTCCGCGACCCCTCCCGGGTCCCGGCCAGCCC 133

QY 121 CTTCCGGGCGCTCCGCGGAGACCCCGCTCTGCTTTCGCGGCGCCGCTCTCTCTCCGCGGCG 180
DB 134 CTTCCGGGCGCTCCGCGGAGACCCCGCTCTGCTTTCGCGGCGCCGCTCTCTCTCCGCGGCG 193

QY 181 CGAGTTTCAGGCGAGCGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 240
DB 194 CGAGTTTCAGGCGAGCGCTGCTGCTGCGACGCTGGGAAGCCCTGGCCCGGCCACCC 253

QY 241 CCGCG 245
DB 254 CCGCG 258

RESULT 4

US-10-863-075-24
Sequence 24, Application US/10863075
Publication No. US2005005962A1
GENERAL INFORMATION:

Query Match	100.0%;	Score 245;	DB 15;	Length 295;
Best Local Similarity	100.0%;	Pred. No. 6.9e-51;		

```

; PRIOR APPLICATION NUMBER: US 60/270,322
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: US 60/295,037
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/348,670
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Viral vector sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(955)
; OTHER INFORMATION: Fig.47. Sequence of the right end of Ar17pAE2fTttx
; US-10-081-969-17

Query Match          100.0%; Score 245; DB 15; Length 955;
Best Local Similarity 100.0%; Pred. No. 4.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1  CCCACGTGGCGGAGGACTGGGACCCGGGCAACCGCTCTGCCCTTCACCTTCCAGCT 60
      |||

```

Db 500 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTCTGCCCCCTTACCTTCCAGCT 441
Qy 61 CCGCTCTCTCGCGCGGACCCCGCCCGCTCCCGGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 440 CCGCTCTCTCGCGCGGACCCCGCCCGCTCCCGGACCCCTCCCGGGTCCCGGGCCAGCCC 381
Qy 121 CCTCGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db 380 CCTCGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 321
Qy 181 CGAGTTTCAGCAGCGTCTGCTCTGTCGACAGTGGAGCCCTGGCCCGGCCACCC 240
Db 320 CGAGTTTCAGCAGCGTCTGCTCTGTCGACAGTGGAGCCCTGGCCCGGCCACCC 261
Qy 241 CCGCG 245
Db 260 CCGCG 256
RESULT 7
US-10-840-455-1
; Sequence 1, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hegen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DE19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 5126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-1
Query Match 100.0%; Score 245; DB 19; Length 5126;
Best Local Similarity 100.0%; Pred. No. 3.1e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTCTGCCCCCTTACCTTCCAGCT 60
Db 4879 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTCTGCCCCCTTACCTTCCAGCT 4938
Qy 61 CCGCTCTCTCGCGCGGACCCCGCCCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 4939 CCGCTCTCTCGCGCGGACCCCGCCCGCTCCCGACCCCTCCCGGGTCCCGGGCCAGCCC 4998
Qy 121 CTTCCGGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db 4999 CTTCCGGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 5058
Qy 181 CGAGTTTCAGGACGCGCTCGTCTGTCGACAGTGGGAAGCCCTTGGCCCGGCCACCC 240
Db 5059 CGAGTTTCAGGACGCGCTCGTCTGTCGACAGTGGGAAGCCCTTGGCCCGGCCACCC 5118
Qy 241 CCGCG 245
Db 5119 CCGCG 5123

RESULT 8

US-09-932-581-25
; Sequence 25, Application US/09932581
; Publication No. US20030050264A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932,581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5928
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
US-09-932-581-25
Query Match 100.0%; Score 245; DB 10; Length 5928;
Best Local Similarity 100.0%; Pred. No. 2.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTCTGCCCCCTTACCTTCCAGCT 60
Db 51 CCCACGTGGCGGAGGACTGGGACCCGGGACCCCGTCTCTGCCCCCTTACCTTCCAGCT 110
Qy 61 CCGCTCTCTCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCAGCCC 120
Db 111 CCGCTCTCTCGCGCGGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCAGCCC 170
Qy 121 CTTCCGGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 180
Db 171 CTTCCGGGGCCCTCCAGCCCTCCCTTCTCTTTCGGGGCCCGCCCTCTCTCTCGGGCG 230
Qy 181 CGAGTTTCAGGACGCGCTCGTCTGTCGACAGTGGGAAGCCCTTGGCCCGGCCACCC 240
Db 231 CGAGTTTCAGGACGCGCTCGTCTGTCGACAGTGGGAAGCCCTTGGCCCGGCCACCC 290
Qy 241 CCGCG 245
Db 291 CCGCG 295

RESULT 9
US-10-338-294-25
; Sequence 25, Application US/10338294
; Publication No. US20030171326A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/10/338,294
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US/09/932,581
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174

RESULT 12

US-10-840-455-43
; Sequence 43, Application US/10840455
; Publication No. US20050032094A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hegen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic
; FILE OF INVENTION: Telomerase Subunit, and Their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805C1
; CURRENT APPLICATION NUMBER: US/10/840,455
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: DB19757984.1
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 26414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-840-455-43

Query Match 100.0%; Score 245; DB 19; Length 26414;
Best Local Similarity 100.0%; Pred. No. 1.9e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGTCGCGGAGGACTGGGGACCCGGGCACCGGTCTCTGCCCCCTTCCACCTTCCAGCT 60
DB 11029 CCCACGTCGCGGAGGACTGGGGACCCGGGCACCGGTCTCTGCCCCCTTCCACCTTCCAGCT 11088

QY 61 CCGCTCTCTCCGCGGAGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCCAAGCCC 120
DB 11089 CCGCTCTCTCCGCGGAGACCCCGCCCGTCCCGACCCCTCCCGGGTCCCGGGCCCAAGCCC 11148

QY 121 CTTCCGGGCTCCCGACGCTCCCTCTCTTCCGCGGCGCCGCTCTCTCGGGGG 180
DB 11149 CTTCCGGGCTCCCGACGCTCCCTCTCTTCCGCGGCGCCGCTCTCTCGGGGG 11208

QY 181 CGAGTTTCAGGACGCTCGGTCTCTGCGCAGTGGGAAGCCCTGGCCCGGCCACCC 240
DB 11209 CGAGTTTCAGGACGCTCGGTCTCTGCGCAGTGGGAAGCCCTGGCCCGGCCACCC 11268

QY 241 CCGCG 245
DB 11269 CCGCG 11273

RESULT 13

US-09-733-294A-30
; Sequence 30, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 30
; LENGTH: 51552
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: exon
; LOCATION: (1)...(11492)
; OTHER INFORMATION: exon 1
; NAME/KEY: intron
; LOCATION: (11493)...(11596)
; OTHER INFORMATION: intron 1
; NAME/KEY: exon
; LOCATION: (11597)...(12950)
; OTHER INFORMATION: exon 2
; NAME/KEY: intron
; LOCATION: (12951)...(21566)
; OTHER INFORMATION: intron 2
; NAME/KEY: exon
; LOCATION: (21567)...(21762)
; OTHER INFORMATION: exon 3
; NAME/KEY: intron
; LOCATION: (21763)...(23851)
; OTHER INFORMATION: intron 3
; NAME/KEY: exon
; LOCATION: (23852)...(24032)
; OTHER INFORMATION: exon 4
; NAME/KEY: intron
; LOCATION: (24033)...(24719)
; OTHER INFORMATION: intron 4
; NAME/KEY: exon
; LOCATION: (24720)...(24899)
; OTHER INFORMATION: exon 5
; NAME/KEY: intron
; LOCATION: (24900)...(25393)
; OTHER INFORMATION: intron 5
; NAME/KEY: exon
; LOCATION: (25394)...(25549)
; OTHER INFORMATION: exon 6
; NAME/KEY: intron
; LOCATION: (25550)...(30196)
; OTHER INFORMATION: intron 6
; NAME/KEY: exon
; LOCATION: (30195)...(30292)
; OTHER INFORMATION: exon 7
; NAME/KEY: intron
; LOCATION: (30293)...(31272)
; OTHER INFORMATION: intron 7
; NAME/KEY: exon
; LOCATION: (31273)...(31358)
; OTHER INFORMATION: exon 8
; NAME/KEY: intron
; LOCATION: (31359)...(33843)
; OTHER INFORMATION: intron 8
; NAME/KEY: unsure
; LOCATION: 31450
; OTHER INFORMATION: unknown
; NAME/KEY: exon
; LOCATION: (33844)...(33957)
; OTHER INFORMATION: exon 9
; NAME/KEY: intron
; LOCATION: (33958)...(35941)
; OTHER INFORMATION: intron 9
; NAME/KEY: exon
; LOCATION: (35942)...(36013)
; OTHER INFORMATION: exon 10
; NAME/KEY: intron
; LOCATION: (36014)...(37884)
; OTHER INFORMATION: intron 10
; NAME/KEY: exon
; LOCATION: (37885)...(38073)
; OTHER INFORMATION: exon 11
; NAME/KEY: intron
; LOCATION: (38074)...(41874)
; OTHER INFORMATION: intron 11
; NAME/KEY: exon
; LOCATION: (41875)...(42001)
; OTHER INFORMATION: exon 12

```
; NAME/KEY: intron
; LOCATION: (42002)...(42881)
; OTHER INFORMATION: intron 12
; NAME/KEY: exon
; LOCATION: (42882)...(42943)
; OTHER INFORMATION: exon 13
; NAME/KEY: intron
; LOCATION: (42944)...(46129)
; OTHER INFORMATION: intron 13
; NAME/KEY: exon
; LOCATION: (46130)...(46254)
; OTHER INFORMATION: exon 14
; NAME/KEY: intron
; LOCATION: (46255)...(47035)
; OTHER INFORMATION: intron 14
; NAME/KEY: exon
; LOCATION: (47036)...(47173)
; OTHER INFORMATION: exon 15
; NAME/KEY: intron
; LOCATION: (47174)...(47709)
; OTHER INFORMATION: intron 15
; NAME/KEY: exon
; LOCATION: (47710)...(50544)
; OTHER INFORMATION: exon 16
US-09-294A-30

Query Match          100.0%; Score 245; DB 9; Length 51552;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGTTGGGGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 60
DB 11029 CCCACGTTGGGGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 11088

QY 61 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 120
DB 11089 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 11148

QY 121 CTCCGGGCGCTCCAGCGCCCTCCCTCTCTTCCGGCGCGCCCGCCCTCTCTCGCGGG 180
DB 11149 CTCCGGGCGCTCCAGCGCCCTCCCTCTCTTCCGGCGCGCCCGCCCTCTCTCGCGGG 11208

QY 181 CGAGTTTCAGGACGCGCTGCGTCTGCTGCGACCTGGGAAGCCCTGGCCCGGCCACCC 240
DB 11209 CGAGTTTCAGGACGCGCTGCGTCTGCTGCGACCTGGGAAGCCCTGGCCCGGCCACCC 11268

QY 241 CGCG 245
DB 11269 CGCG 11273

RESULT 14
US-10-674-836-17
; Sequence 17, Application US/10674836
; Publication No. US20040072787A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vassebot, Alain
; APPLICANT: Adams, Robert R.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Telomerase Reverse Transcriptase Transcriptional
; FILE REFERENCE: 019/246P
; CURRENT APPLICATION NUMBER: US/10/674,836
; CURRENT FILING DATE: 2003-09-29
; PRIOR FILING DATE: US/09/244,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 298
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TERT promoter
US-10-674-836-17

Query Match          99.6%; Score 244; DB 17; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCTC 61
DB 52 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCTC 111

QY 62 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 121
DB 112 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 171

QY 122 CTCCGGGCGCTCCAGCGCCCTCCCTCTCTTCCGGCGCGCCCGCTCTCTCGGGGGC 181
DB 172 CTCCGGGCGCTCCAGCGCCCTCCCTCTCTTCCGGCGCGCCCGCTCTCTCGGGGGC 231

QY 182 GAGTTTCAGGACGCGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 241
DB 232 GAGTTTCAGGACGCGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 291

QY 242 CGCG 245
DB 292 CGCG 295

RESULT 15
US-10-212-667-1
; Sequence 1, Application US/10212667
; Publication No. US20030082722A1
; GENERAL INFORMATION:
; APPLICANT: FANG, BIANGLIANG
; TITLE OF INVENTION: METHOD FOR AMPLIFYING EXPRESSION FROM A CELL SPECIFIC
; FILE REFERENCE: UTSC:708US
; CURRENT APPLICATION NUMBER: US/10/212,667
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: 60/310,905
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-212-667-1

Query Match          99.6%; Score 244; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.1e-50;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 60
DB 135 CCCACGTGGCGAGGAGCTGGGGACCCCGGGACCCGCTCTGCGCCCTTCACTTCCAGCT 194

QY 61 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 120
DB 195 CGCCTCTCTCGCGGGACCCCGCGCTCCCGACCCCTCCCGGTCCCGGCCCGAGCCC 254

QY 121 CCTCGGGCGCTTCCAGCGCCCTCCCTCTCTTCCCGCGGCCCGCCCTCTCTCTCGGGCG 180
DB 255 CCTCGGGCGCTTCCAGCGCCCTCCCTCTCTTCCCGCGGCCCGCCCTCTCTCTCGGGCG 314

QY 181 CGAGTTTCAGGACGCGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 240
DB 315 CGAGTTTCAGGACGCGCTGCGTCTGCTGCGACGTTGGGAAGCCCTGGCCCGGCCACCC 374
```

Qy 241 CCGC 244
Db 375 CCGC 378

Search completed: April 9, 2005, 10:41:31
Job time : 314.31 secs